

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:52 ; Search time 147.68 seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 taaggcgttcgataaaccc 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents_NA: *
1: /cgn2_6/ptodata/2/lna/5A.COMB.seq: *
2: /cgn2_6/ptodata/2/lna/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/lna/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/lna/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/lna/PCRTS.COMB.seq: *
6: /cgn2_6/ptodata/2/lna/Backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	432	US-08-313-185-59	Sequence 59, Appl
2	20	100.0	432	US-09-082-614A-59	Sequence 59, Appl
3	20	100.0	620	US-08-757-653-135	Sequence 135, App
4	20	100.0	620	US-08-757-653-136	Sequence 136, App
5	20	100.0	620	US-08-757-653-137	Sequence 137, App
6	20	100.0	620	US-08-757-653-138	Sequence 138, App
7	20	100.0	620	US-08-757-653-139	Sequence 139, App
8	20	100.0	620	US-08-757-653-140	Sequence 140, App
9	20	100.0	706	US-08-797-812-24	Sequence 24, Appl
10	20	100.0	970	US-08-250-030-1	Sequence 1, Appl
11	20	100.0	970	PCT-US95-06790-1	Sequence 1, Appl
12	19	95.0	19	US-08-750-088A-71	Sequence 71, Appl
13	15	75.0	27	US-08-250-030-9	Sequence 9, Appl
14	15	75.0	27	PCT-US95-06790-9	Sequence 9, Appl
15	14	70.0	3447	US-08-313-185-57	Sequence 57, Appl
16	14	70.0	3447	US-09-082-614A-57	Sequence 57, Appl
17	13	65.0	383	US-08-906-769-169	Sequence 169, App
18	13	65.0	383	US-08-906-769-169	Sequence 169, App
19	13	65.0	383	US-08-906-769-169	Sequence 169, App
20	13	65.0	383	US-08-639-075A-169	Sequence 169, App
21	13	65.0	383	US-09-012-431-169	Sequence 169, App
22	13	65.0	383	US-09-012-692-169	Sequence 169, App
23	13	65.0	537	US-08-906-613-169	Sequence 169, App
24	13	65.0	537	US-08-906-769-171	Sequence 171, App
25	13	65.0	537	US-08-906-616-171	Sequence 171, App
26	13	65.0	537	US-08-639-075A-171	Sequence 171, App
27	13	65.0	537	US-09-012-431-171	Sequence 171, App
28	13	65.0	537	US-09-012-692-171	Sequence 171, App

28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, Appl
30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, Appl
31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, Appl
32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, Appl
33	13	65.0	3000	2	US-09-360-682A-1	Sequence 1, Appl
34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, Appl
35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, Appl
36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, Appl
37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
38	12	60.0	391	1	US-08-636-928-6	Sequence 6, Appl
39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
40	12	60.0	645	1	US-08-459-586-19	Sequence 19, Appl
41	12	60.0	645	2	US-08-282-696-19	Sequence 19, Appl
42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, Appl
43	12	60.0	709	1	US-08-459-586-20	Sequence 20, Appl
44	12	60.0	709	2	US-08-282-696-20	Sequence 20, Appl
45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/C
Sequence 59, Application US/08313185
Patent No. 5831763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunne
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 428 TACGGCGCTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/c

; Sequence 59, Application US/09082614A

; Patent No. 6124098

; GENERAL INFORMATION:

; APPLICANT: Heym, Beate

; APPLICANT: Cole, Stewart

; APPLICANT: Young, Douglas

; APPLICANT: Zhang, Ying

; APPLICANT: Honore, Nadine

; APPLICANT: Telenti, Amalio

; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082.614A

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US 08/313,185

; FILING DATE: 12-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 428 TACGGCGCTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/c

; Sequence 135, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medien & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medien & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757.653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 135:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 620 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
|||||
DB 296 TACGGCGCTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/c

; Sequence 136, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medien & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/C
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FONS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-139

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 620;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
US-08-757-653-140
Sequence 140 Application US/08757653
Patent No. 5843869
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FONS-02565
```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-140

Query Match
Best Local Similarity 100.0%; Score 20; DB 2; Length 620;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
US-08-797-812-24/C
Sequence 24 Application US/08797812
Patent No. 6228575
GENERAL INFORMATION:
APPLICANT: Gingeras, Thomas A.
APPLICANT: Mack, David
APPLICANT: Chee, Mark S.
APPLICANT: Beruo, Anthony J.
APPLICANT: Stryer, Lubert
APPLICANT: Ghandour, Ghassan
APPLICANT: Wang, Ching
TITLE OF INVENTION: Chip-Based Species Identification and
TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,812
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,339
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Filts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 16528X-018550
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 24:
```


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130:219116

TI Method of selecting PCR primer pairs to amplify a group of related nucleotide sequences

IN McClelland, Michael; Pesole, Graziano

PA Sidney Kimmel Cancer Center, USA

SO PCT Int. Appl., 92 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9911823	A2	19990311	WO 1998-US18392	19980904
	WO 9911823	A3	19990610		
	W:	AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
	AU 9893027	A1	19990322	AU 1998-93027	19980904
	EP 1007739	A2	20000614	EP 1998-945882	19980904
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI			
PRAI	US 1997-925816	A	19970905		
	WO 1998-US18392	W	19980904		
AB	The present invention provides a method of detg. a set of primer pairs for amplifying a group of related nucleotide sequences. A method of the invention is performed by identifying a group of related nucleotide sequences; generating the set of primers that matches each of the related nucleotide sequences; detg. for each systematic pairing of each primer which of the related nucleotide sequences are amplified; and selecting from the systematic pairings a subset which amplifies all of the related nucleotide sequences. The invention also provides a method of using a set of primer pairs, which amplify a group of related nucleotide sequences, to identify nucleotide sequences related to the original group of nucleotide sequences. Eight-mer primer pairs are provided for amplification of genes encoding nuclear receptors, G-protein coupled receptors, apoptosis-assocd. proteins, DNA repair enzymes, and replication enzymes. The invention also provides a computer app. for carrying out the computer-executed steps of the method. The invention further provides a computer program product comprising a signal bearing media for carrying out the method.				

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723

GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:

APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138

GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/750,088A
;; FILING DATE: 21-FEB-1997
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: GOLDSTEIN, JORGE A.
;; REGISTRATION NUMBER: 29,021
;; REFERENCE/DOCKET NUMBER: 1657.0010000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 71:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-750-088A-71

Query Match 95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 19
Db 1 TACGGCGTTTCGATGAACC 19

RESULT 13
US-08-250-030-9
; Sequence 9, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-250-030-9

Query Match 75.0%; Score 15; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaacc 20
Db 1 CGTTTCGATGAACC 15

RESULT 14
PCT-US95-06790-9
; Sequence 9, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105W01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US95-06790-9

Query Match 75.0%; Score 15; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaacc 20
Db 1 CGTTTCGATGAACC 15

RESULT 15
US-08-313-185-57/c
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 70.0%; Score 14; DB 2; Length 3447;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 gttcgatgaacc 20
|||||
Db 1448 GTTCGATGAACCC 1435

Search completed: August 7, 2002, 23:51:54
Job time: 7180 sec



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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:31 ; Search time 562.71 Seconds
(Without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 tacgctgcgcgcgcgcgcgcgc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AA112092	M. tuberculosis rp
2	20	100.0	20	AAA49823	Mycobacterium tube
3	20	100.0	20	AAA49825	Mycobacterium tube
4	20	100.0	306	AAK27214	RpoB gene fragment
5	20	100.0	306	AAK27175	RpoB gene fragment
6	20	100.0	306	AAK27179	RpoB gene fragment
7	20	100.0	306	AAK27180	RpoB gene fragment
8	20	100.0	306	AAK27180	Mycobacterium spec
9	20	100.0	306	AAK27180	Mycobacterium spec

10	20	100.0	306	24	AAK27180	Mycobacterium spec
11	20	100.0	306	24	AAK27180	Mycobacterium spec
12	20	100.0	432	14	AAK27180	Mycobacterium spec
13	20	100.0	480	21	AAK27180	Mycobacterium spec
14	20	100.0	970	17	AAK27180	Mycobacterium spec
15	20	100.0	3519	22	AAK27180	Mycobacterium spec
16	20	100.0	3534	22	AAK27180	Mycobacterium spec
17	20	100.0	3853	21	AAK27180	Mycobacterium spec
18	20	100.0	3853	21	AAK27180	Mycobacterium spec
19	20	100.0	3853	21	AAK27180	Mycobacterium spec
20	20	100.0	3853	21	AAK27180	Mycobacterium spec
21	20	100.0	3853	21	AAK27180	Mycobacterium spec
22	20	100.0	3853	21	AAK27180	Mycobacterium spec
23	20	100.0	3853	21	AAK27180	Mycobacterium spec
24	20	100.0	3853	21	AAK27180	Mycobacterium spec
25	20	100.0	3853	21	AAK27180	Mycobacterium spec
26	20	100.0	3853	21	AAK27180	Mycobacterium spec
27	20	100.0	3853	21	AAK27180	Mycobacterium spec
28	20	100.0	3853	21	AAK27180	Mycobacterium spec
29	20	100.0	3853	21	AAK27180	Mycobacterium spec
30	20	100.0	3853	21	AAK27180	Mycobacterium spec
31	20	100.0	3853	21	AAK27180	Mycobacterium spec
32	20	100.0	3853	21	AAK27180	Mycobacterium spec
33	20	100.0	3853	21	AAK27180	Mycobacterium spec
34	20	100.0	3853	21	AAK27180	Mycobacterium spec
35	20	100.0	3853	21	AAK27180	Mycobacterium spec
36	20	100.0	3853	21	AAK27180	Mycobacterium spec
37	20	100.0	3853	21	AAK27180	Mycobacterium spec
38	20	100.0	3853	21	AAK27180	Mycobacterium spec
39	20	100.0	3853	21	AAK27180	Mycobacterium spec
40	20	100.0	3853	21	AAK27180	Mycobacterium spec
41	20	100.0	3853	21	AAK27180	Mycobacterium spec
42	20	100.0	3853	21	AAK27180	Mycobacterium spec
43	20	100.0	3853	21	AAK27180	Mycobacterium spec
44	20	100.0	3853	21	AAK27180	Mycobacterium spec
45	20	100.0	3853	21	AAK27180	Mycobacterium spec

ALIGNMENTS

RESULT 1	
ID	AA112092
10-JUN-1996	(first entry)
AC	AA112092:
DT	10-JUN-1996 (first entry)
DE	M. tuberculosis rpoB gene fragment amplification primer P2.
XX	Antibiotic: resistance; spectrum: gene: mycobacterium;
KW	determination: amplification: tuberculosis; rpoB; fragment;
KW	primer: differential; hybridisation; pattern; rifampicin;
KW	rifampicin; species identification; ss.
XX	Synthetic.
XX	MO538851-A2
PN	14-DEC-1995.
PD	09-JUN-1995; 95WO-EP02230.
PE	09-JUN-1995; 95WO-EP02230.
PR	09-JUN-1994; 94EP-0870093.
PA	(INNO-) INNOGENETICS NV.
PI	De Beenhouwer H, Jannes G, Machtelinkx L, Portaeals F;
PI	Rosau R;
XX	WPI: 1996-040250/04.
DR	
XX	

PT Probes and primers for determ. of antibiotic resistance spectrum of
 PT *Mycobacterium*, opt. coupled with species identification - from
 XX different patterns of hybridisation with rpoB gene
 PS
 PV Claim 22: Page 39, 69pp; English.

The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the *M. tuberculosis* rpoB gene fragment amplified using the primer set AAT12091-98, hybridising it with at least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is particularly useful for the detection of rifampicin and/or rifabutin resistance in *M. leprae* or *M. tuberculosis*, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determination of ARS and spp. identity.

Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match	100.0%	Score 20;	DB 17;	Length 20;
Best Local Similarity	100.0%	Pred. No. 0.031;		
Matches	20;	Conservative 0;	Mismatches 0.	Indels 0.

QY		1	tacggtcgcgcgagctgatcc	20
Dd		1	tacggtcgcgcgagctgatcc	20

RESULT	2
AAA49823	
ID	AAA49823 standard; DNA; 20 BP.
vv	

DT 25-SEP-2000 (first entry)
 YY

Myco bacterium tuberculosis rpoB gene amplification primer rpoB-F.

..... resistance; rpoB gene; rifampin resistance; PCR primer;
ss,

Mycobacterium tuberculosis.

PN WO200036142-A1

PD 22-JUN-2000.

10-DEC-1999; 99WO-CA01177.

11-DEC-1998; 98US-0111794.

(VISI-) VISIBLE GENETICS INC.

Shlpmn R

WPI; 2000-431611/37.

tuberculosis with antibiotic resistance in a sample -

Claim 4; Page 4; 43pp; English.

The present sequence is that of the *Mycobacterium tuberculosis* rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-2220). It is used with the reverse primer given in AAA49824 and with the sequencing primers given in AAA49825 and AAA49826 for the detection and analysis of rifampin resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-phc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (chloramphenicol) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the presence of *M.*
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other.

Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match	100.0%;	Score 20;	DB 21;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 0.031;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	tacggtcggcgagctgacc	20
Dbb	1	tacggtcggcgagctgacc	20

RESULT	3
AAA49825	
ID	AAA49825 standard; DNA; 20 BP.
XY	

AC AAA49825;

DT 25-SEP-2000 (first entry)
 YY

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX

resistance; rpoB gene; rifampin resistance; primer; ss.

05 *Mycobacterium tuberculosis*.

PN WO2000036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VIST-) VISIBLE GENETICS INC.

PI Shipman R;
xy

WPI; 2000-431611/37.

Method for the detection and characterization of *Mycobacterium tuberculosis* with antibiotic resistance in a sample -

The present sequence is that of

The present sequence is that of the *Mycobacterium tuberculosis* *rrpB* (rifampin resistance) gene sequencing primer *rrpB*-5s (bp 2201-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the *rrpB* gene (see AAA49833). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of *rrpB* (rifampin), *katG* (isoniazid), *oxyR*-apc PR (isoniazid), *mabA* (isoniazid), *rpsL*/312 (streptomycin), 16S/rrs (streptomycin), *embB* (ethambutol), *pncA* (pyrazinamide), *gyrA* (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpoB*, *katG*, *IS*₆₁₁₀
CC and 235 genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

XX
XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcgtgatcc 20
|||||
DB 1 tacggtcgagcgtgatcc 20

RESULT 4

AAx27214
ID AAX27214 standard; DNA; 306 BP.

XX
XX AAX27214;

XX
XX 27-MAY-1999 (first entry)

DE RpoB gene fragment.

XX RpoB gene; mycobacteria; phylogenetic tree construction;

KW mycobacterial species identification; phylogenetic analysis; ss.

XX
XX Mycobacteria tuberculosis.

OS
XX W09905316-A1.

PN
XX 04-FEB-1999.

XX
XX 28-JUL-1998; 98KR-0000228.

PF
XX 28-JUL-1997; 97KR-0035501.

PR
XX (BION-) BIONEER CORP.

PA
XX Kim B, Kook Y;

PI
XX WPI: 1998-539367/46.

DR
XX New pair of polymerase chain reaction (PCR) primers - for

XX sequence-specific amplification of the *rpoB* gene from mycobacterial

PT species, useful for detecting and identifying mycobacterial species

PS Claim 43; Page 75-76; 91pp; English.

XX
XX This sequence represents a mycobacterial *rpoB* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpoB* gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterizing these species. In addition to
CC phylogenetic analysis, the *rpoB* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.

XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcgtgatcc 20
|||||
DB 5 tacggtcgagcgtgatcc 24

RESULT 5

AAx27175
ID AAX27175 standard; DNA; 306 BP.

XX
XX AAX27175;

XX
XX 27-MAY-1999 (first entry)

DE RpoB gene fragment.

XX RpoB gene; mycobacteria; phylogenetic tree construction;

KW mycobacterial species identification; phylogenetic analysis; ss.

XX
XX Mycobacteria africanum.

OS
XX W09905316-A1.

PN
XX 04-FEB-1999.

XX
XX 28-JUL-1998; 98KR-0000228.

PF
XX 28-JUL-1997; 97KR-0035501.

PR
XX (BION-) BIONEER CORP.

PA
XX Kim B, Kook Y;

PI
XX WPI: 1998-539367/46.

DR
XX New pair of polymerase chain reaction (PCR) primers - for

XX sequence-specific amplification of the *rpoB* gene from mycobacterial

PT species, useful for detecting and identifying mycobacterial species

PS Claim 4; Page 62-63; 91pp; English.

XX
XX This sequence represents a mycobacterial *rpoB* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpoB* gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterizing these species. In addition to
CC phylogenetic analysis, the *rpoB* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.

XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcgtgatcc 20
|||||
DB 5 tacggtcgagcgtgatcc 24

RESULT 6

AAx27179

```

ID  AAX27179 standard; DNA; 306 BP.
XX
XX  AAX27179;
AC
XX  27-MAY-1999 (first entry)
DT
XX
XX  RPOB gene fragment.
DE
XX
XX  RPOB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
XX  Mycobacteria bovis.
OS
XX
XX  WO905316-A1.
PN
XX
XX  04-FEB-1999.
PD
XX
XX  28-JUL-1998; 98KR-0000228.
PF
XX
XX  28-JUL-1997; 97KR-0035501.
PR
XX
XX  (BION-) BIONEER CORP.
PA
XX
XX  Kim B, Kook Y;
PI
XX
XX  WPI; 1998-539367/46.
DR
XX
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
XX
XX  Claim 8; Page 64; 91pp; English.
PS
XX
XX  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterising these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX  Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
SQ

Query Match          100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1  tacggtcggcgagctgatcc 20
    |||
DB  5  tacggtcggcgagctgatcc 24

RESULT 7
AAX27180
ID  AAX27180 standard; DNA; 306 BP.
XX
XX  AAX27180;
AC
XX
XX  27-MAY-1999 (first entry)
DT
XX
XX  RPOB gene fragment.
DE
XX
XX  RPOB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
XX  Mycobacteria bovis.
OS
XX

```

```

PN  WO905316-A1.
XX
XX  04-FEB-1999.
PD
XX
XX  28-JUL-1998; 98KR-0000228.
PF
XX
XX  28-JUL-1997; 97KR-0035501.
PR
XX
XX  (BION-) BIONEER CORP.
PA
XX
XX  Kim B, Kook Y;
PI
XX
XX  WPI; 1998-539367/46.
DR
XX
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PT  species, useful for detecting and identifying mycobacterial species
XX
XX  Claim 9; Page 64; 91pp; English.
PS
XX
XX  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterising these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX  Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

Query Match          100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  1  tacggtcggcgagctgatcc 20
    |||
DB  5  tacggtcggcgagctgatcc 24

RESULT 8
AAS99526
ID  AAS99526 standard; DNA; 306 BP.
XX
XX  AAS99526;
AC
XX
XX  12-MAR-2002 (first entry)
DT
XX
XX  Mycobacterium species identification primer #1.
DE
XX
XX  Drug resistance detection; mycobacterial species identification; probe;
KM  oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX  primer.
XX
XX  Mycobacterium tuberculosis.
OS
XX
XX  WO200192573-A1.
PN
XX
XX  06-DEC-2001.
PD
XX
XX  30-MAY-2001; 2001MO-KR00904.
PF
XX
XX  30-MAY-2000; 2000KR-0029369.
PR
XX
XX  (BION-) BIOMEDIAB CO LTD.
PA
XX
XX  Kim H, Kim N, Yoon S, Kim J, Park M;
PI
XX

```

DR	WPI: 2002-075472/10.
XX	
PT	Kit for mycobacterial species identification and drug resistance
PR	detection, has oligonucleotide chip with species identification probe,
PT	a mycobacterial drug-resistance detection probe, and its contrast group
PT	probe -
XX	
PS	Disclosure: Page 21; 74pp; English.
XX	
CC	The invention relates to a diagnostic kit for mycobacterial species
CC	identification and drug resistance detection comprising an
CC	oligonucleotide chip including a species identification probe, a
CC	mycobacterial drug-resistance detection probe, a contrast group probe
CC	corresponding to each drug resistance detection probe, and a marker for
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC	identification probe is comprised of species-specific DNA sequences of
CC	mycobacterial rpoB gene and the detection probe is comprised of one or
CC	more modified codons of mycobacterial rpoB gene. The method involves
CC	amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC	(PCR) and discriminating species by fluorescent intensity corresponding
CC	to a particular species. The specimen is preferably uncultured sputum,
CC	blood or cerebrospinal fluid of a patient. Sequences AAS9478-AAS9569
CC	represent mycobacterium species identification probes and primers of the
CC	invention.
SQ	
XX	Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
XX	
Query Match	100.0%; Score 20; DB 24; Length 306;
Best Local Similarity	100.0%; Pred. No. 0.025;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	
1 tacggcgcgagactgatcc 20	
Db 5 tacggtcgcgcgagctgatcc 24	
RESULT 9	
AAS9527	
ID AAS9527 standard; DNA; 306 BP.	
XX	
AC AAS9527;	
XX	
DT 12-MAR-2002 (first entry)	
XX	
DE Mycobacterium species identification primer #2.	
XX	
KM Drug resistance detection: mycobacterial species identification probe;	
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;	
KM primer.	
XX	
OS Mycobacterium africanum.	
OS	
PN WO200192573-A1.	
XX	
PD 06-DEC-2001.	
XX	
PF 30-MAY-2001; 2001WO-KR00904.	
XX	
PR 30-MAY-2000; 2000KR-0029369.	
XX	
PA (BIOM-) BIOMEDLAB CO LTD.	
XX	
P1 Kim H, Kim N, Yoon S, Kim J, Park M;	
XX	
DR WPI: 2002-075472/10.	
XX	
PT Kit for mycobacterial species identification and drug resistance	
PT	detection, has oligonucleotide chip with species identification probe,
PT	a mycobacterial drug-resistance detection probe, and its contrast group
PT	probe -
XX	
XS Disclosure; Page 21; 74pp; English.	

XX	The invention relates to a diagnostic kit for mycobacterial species
CC	identification and drug resistance detection comprising an
CC	oligonucleotide chip including a species identification probe, a
CC	mycobacterial drug-resistance detection probe, a contrast group probe
CC	corresponding to each drug resistance detection probe, and a marker for
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC	identification probe is comprised of species-specific DNA sequences of
CC	mycobacterial rpoB gene and the detection probe is comprised of one or
CC	more modified codons of mycobacterial rpoB gene. The method involves
CC	amplifying rpoB gene fragments of specimen by polymerase chain reaction
CC	(PCR), and discriminating species by fluorescent intensity corresponding
CC	to a particular species. The specimen is preferably uncultured sputum,
CC	blood or cerebrospinal fluid of a patient. Sequences AAS9478-AAS9569
CC	represent mycobacterium species identification probes and primers of the
CC	invention.
XX	
SQ	Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
OY	1 tacgctcgcgcagactgatcc 20
DB	
	5 tacggctcgcgagctgatcc 24
RESULT	10
AAS99530	.
ID	AAS99530 standard; DNA; 306 BP.
AC	AAS99530;
DT	12-MAR-2002 (first entry)
DE	Mycobacterium species identification primer #5.
KW	Drug resistance detection; mycobacterial species identification; probe;
KM	oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX	primer.
OS	Mycobacterium bovis.
PN	WO200192573-A1.
PD	06-DEC-2001.
PF	30-MAY-2001; 2001WO-KR00904.
PR	30-MAY-2000; 2000KR-0029369.
PA	(BIOM-) BIOMEDLAB CO LTD.
PI	Kim H, Kim N, Yoon S, Kim J, Park M;
DR	WPI: 2002-075472/10.
XX	
PT	Kit for mycobacterial species identification and drug resistance
PT	detection, has oligonucleotide chip with species identification probe, a
PT	mycobacterial drug-resistance detection probe, and its contrast group
XX	probe -
PS	Disclosure: Page 21; 74pp; English.
XX	
CC	The invention relates to a diagnostic kit for mycobacterial species
CC	identification and drug resistance detection comprising an
CC	oligonucleotide chip including a species identification probe, a
CC	mycobacterial drug-resistance detection probe, a contrast group probe
CC	corresponding to each drug resistance detection probe, and a marker for
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC	identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgagcagctgatcc 20
|||||
Db 5 tacgctcgagcagctgatcc 24

RESULT 11
AAS99531

ID AAS99531 standard; DNA; 306 BP.

XX AAS99531;

DT 12-MAR-2002 (first entry)

DE Mycobacterium species identification primer #6.

KW Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX primer.

OS Mycobacterium bovis.

PN WO200192573-A1.

PD 06-DEC-2001.

PF 30-MAY-2001; 2001WO-KR00904.

PR 30-MAY-2000; 2000KR-0029369.

PA (BIOM-) BIOMEDLAB CO LTD.

PI Kim H, Kim N, Yoon S, Kim J, Park M;

DR WPI; 2002-075472/10.

PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX

PS Disclosure; Page 21; 74pp; English.

XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.

XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgagcagctgatcc 20
|||||
Db 5 tacgctcgagcagctgatcc 24

RESULT 12
AAQ61457

ID AAQ61457 standard; DNA; 432 BP.

XX AAQ61457;

DT 17-MAY-1994 (first entry)

DE M.tuberculosis rpoB gene fragment.

KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.

OS Mycobacterium tuberculosis.

PN WO9322454-A.

PD 11-NOV-1993.

PF 30-APR-1993; 93WO-EP01063.

PR 17-SEP-1992; 92FR-0011098.

PR 30-APR-1992; 92US-0875940.

PR 14-AUG-1992; 92US-0929206.

PR 16-APR-1993; 93FR-0004545.

PA (ASSI-) ASSISTANCE PUBLIQUE.

PA (INST PASTEUR.

PA (MEDIT-) MEDICAL RES COUNCIL.

PA (UYBE-) UNIV BERN.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;

PI Young D, Zhang Y;

DR WPI; 1993-368812/46.

DR P-PsDB; AARS1372.

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX

PS Example 2; Fig 13; 97pp; English.

XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AAQ61457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX

SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctcgagcagctgatcc 20

```
Db 18 tacggtcgagcgtcatcc 37
|||||
RESULT 13
AAA49863
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind /tag= a
FT /note= "primer of AAA49823"
FT primer_bind /tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
FT Method for the detection and characterization of Mycobacterium
FT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure: Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;
Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
0Y 1 tacggtcgagcgtcatcc 20
```

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Db 41 tacggtcgagcgtcatcc 60
|||||
RESULT 14
AAT09676
ID AAT09676 standard; DNA; 970 BP.
XX
AC AAT09676;
XX
DT 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
XX polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind 10..27
FT /tag= a
FT /note= "primer FENLFF"
FT primer_bind 226..243
FT /tag= b
FT /note= "primer DDIDHL"
FT primer_bind 226..240
FT /tag= c
FT /note= "primer DDIDH"
FT primer_bind 338..364
FT /tag= d
FT /note= "primer rpo95"
FT primer_bind 348..373
FT /tag= e
FT /note= "primer rpo105"
FT primer_bind 354..373
FT /tag= f
FT /note= "primer KY290"
FT misc_feature 372..373
FT /tag= g
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 433..434
FT /tag= h
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 438
FT /tag= i
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 468..469
FT /tag= j
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 486
FT /tag= k
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 501
FT /tag= l
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 516
FT /tag= m
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 516..535
FT /tag= n
FT /note= "primer rpo273"
FT misc_feature 525
FT /tag= o
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 525..541
FT /tag= p
FT /note= "primer KY292"
FT primer_bind 536..562
FT /tag= q
FT /note= "primer rpo293"
FT primer_bind 640..666
FT /tag= r
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FT primer_bind /note="primer rpo397"
FT 952..966
FT /*tag= s
FT /note="primer NMORO-1"
FT primer_bind 952..966
FT /*tag= t
FT /note="primer NMORO-2"
XX
XX WO9533074-A1.
XX
XX 07-DEC-1995.
XX
XX
XX 26-MAY-1995; 95MO-US06790.
XX
XX 26-MAY-1994; 94US-0250030.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Felmlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX Young KKT;
XX WPI; 1996-030581/03.
XX
XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX with a primer set that targets portions of the gene encoding rpoB.
XX
XX Disclosure; Fig.3; 54pp; English.
XX
XX This oligonucleotide DNA primer is specific for Mycobacterium
XX tuberculosis, and may be used to amplify a sample DNA by targeting
XX a portion of the gene encoding rpoB. The 1st several bases comprise a
XX nonhybridizing tail consisting of filler bases followed by
XX a restriction site incorporated to facilitate cloning using the
XX amplicon at a later date, if desired. The remaining bases hybridize
XX to bacterial rpoB DNA. The method provides for the detection of M.
XX tuberculosis and the concurrent determination of its drug
XX susceptibility, particularly to rifampin. The method can provide
XX often greater than 95% sensitivity and 100% specificity. The
XX biological sample is a fluid or tissue sample from a human.
XX
XX Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 17; Length 970;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tacggtcgcgcgagctgattcc 20
XX |||||||||||||||||||
XX Db 261 tacggtcgcgcgagctgattcc 280
XX
XX
XX RESULT 15
XX AAH51976
XX ID AAH51976 standard; DNA; 3519 BP.
XX
XX AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX OS
XX PN WO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-US31152.
XX

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PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI; 2001-329193/34.
XX
XX P-PSDB; AAG81125.
XX
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
XX involves providing algorithm that analyzes a functional relationship
XX between nucleotide or polypeptide sequences, and comparing the
XX sequences
XX
XX Disclosure; Page 68-69; 207pp; English.
XX
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The
XX method involves providing an unknown nucleotide or polypeptide sequences,
XX and comparing it to a number of sequences along with at least one
XX nucleotide and polypeptide sequences. The method is useful for
XX characterizing the function of nucleic acids and polypeptides that may be
XX useful as a target for a drug or essential for the growth or viability of
XX an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 22; Length 3519;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tacggtcgcgcgagctgattcc 20
XX |||||||||||||||||||
XX Db 1119 tacggtcgcgcgagctgattcc 1138
XX

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:45 ; Search time 147.68 seconds

(without alignments)
33.266 Million cell updates/sec

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Word size : 0

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	432	2 US-08-313-185-59	Sequence 59, Appl
C 2	20	100.0	432	3 US-09-082-614A-59	Sequence 15, Appl
C 3	20	100.0	620	2 US-08-757-653-135	Sequence 135, App
C 4	20	100.0	620	2 US-08-757-653-136	Sequence 136, App
C 5	20	100.0	620	2 US-08-757-653-137	Sequence 137, App
C 6	20	100.0	620	2 US-08-757-653-138	Sequence 138, App
C 7	20	100.0	620	2 US-08-757-653-139	Sequence 139, App
C 8	20	100.0	620	2 US-08-757-653-140	Sequence 140, App
C 9	20	100.0	706	4 US-08-797-812-24	Sequence 24, Appl
C 10	20	100.0	970	1 US-08-250-030-1	Sequence 1, Appl
C 11	20	100.0	970	5 PCT-US95-06790-1	Sequence 1, Appl
C 12	19	95.0	19	4 US-08-750-088A-71	Sequence 71, Appl
C 13	15	75.0	27	1 US-08-250-030-9	Sequence 9, Appl
C 14	15	75.0	27	5 PCT-US95-06790-9	Sequence 9, Appl
C 15	14	70.0	3447	3 US-08-313-185-57	Sequence 57, Appl
C 16	14	70.0	3447	3 US-08-082-614A-57	Sequence 57, Appl
C 17	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
C 18	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
C 19	13	65.0	383	3 US-08-639-075A-169	Sequence 169, App
C 20	13	65.0	383	3 US-08-639-075A-169	Sequence 169, App
C 21	13	65.0	383	4 US-09-012-431-169	Sequence 169, App
C 22	13	65.0	383	4 US-09-012-692-169	Sequence 169, App
C 23	13	65.0	537	3 US-08-906-613-169	Sequence 169, App
C 24	13	65.0	537	3 US-08-906-769-171	Sequence 171, App
C 25	13	65.0	537	3 US-08-906-616-171	Sequence 171, App
C 26	13	65.0	537	4 US-08-639-075A-171	Sequence 171, App
C 27	13	65.0	537	4 US-09-012-431-171	Sequence 171, App

28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, Appl
30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, Appl
31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, Appl
32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, Appl
33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, Appl
34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, Appl
35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, Appl
36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, Appl
37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
38	13	65.0	391	1	US-08-636-928-6	Sequence 123, App
39	12	60.0	412	4	US-08-976-259-123	Sequence 19, Appl
40	12	60.0	645	1	US-08-459-586-19	Sequence 19, Appl
41	12	60.0	645	2	US-08-282-686-19	Sequence 4, Appl
42	12	60.0	648	5	PCT-US96-04648-4	Sequence 20, Appl
43	12	60.0	709	1	US-08-459-586-20	Sequence 20, Appl
44	12	60.0	709	2	US-08-282-696-20	Sequence 615, App
45	12	60.0	728	4	US-08-998-416-615	

ALIGNMENTS

RESULT 1
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Teleni, Amelio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Farbow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313.185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgcttcgatgaacc 20
|||||
Db 428 TACGCGCTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356, 0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgcttcgatgaacc 20
|||||
Db 428 TACGCGCTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669

GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGCGCTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843669
; GENERAL INFORMATION:
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/C
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Medlen & Carroll, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States Of America
;; ZIP: 94104
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,653
;;
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 139:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-757-653-139

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgacc 20
|||||
Db 325 TACGGCGTTTCGATGACCC 344

RESULT 8
US-08-757-653-140
; Sequence 140, Application US/08757653
; Patent No. 5843669
; GENERAL INFORMATION:
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Lyamichev, Natasha
; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
; NUMBER OF SEQUENCES: 190
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States Of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,653
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: FORS-02565

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 140:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-757-653-140

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 taaggcgttcgatgacc 20
|||||
Db 325 TACGGCGTTTCGATGACCC 344

RESULT 9
US-08-797-812-24/C
; Sequence 24, Application US/08797812
; Patent No. 6228575
; GENERAL INFORMATION:
; APPLICANT: Gingeras, Thomas A.
; APPLICANT: Mack, David
; APPLICANT: Chee, Mark S.
; APPLICANT: Berno, Anthony J.
; APPLICANT: Stryer, Lubert
; APPLICANT: Ghandour, Chassan
; APPLICANT: Wang, Ching
; TITLE OF INVENTION: Chip-Based Species Identification and
; TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,812
; FILING DATE: 07-FEB-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/017,765
; FILING DATE: 15-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/629,031
; FILING DATE: 08-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,631
; FILING DATE: 01-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,339
; FILING DATE: 08-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Filts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 16528X-018550
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACCC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723

GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.00053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138

GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657,0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-750-088A-71

Query Match 95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0024;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 19
Db 1 TACGGCGCTTCGATGAACC 19

RESULT 13
US-08-250-030-9
Sequence 9, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150,105051
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-9

Query Match 75.0%; Score 15; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
Db 1 CGTTTCGATGAACC 15

RESULT 14
PCT-US95-06790-9
Sequence 9, Application PC/TUS9506790
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150,105W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-9

Query Match 75.0%; Score 15; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
Db 1 CGTTTCGATGAACC 15

RESULT 15
US-08-313-185-57/C
Sequence 57, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

;; TITLE OF INVENTION: In Mycobacterium Tuberculosis
;; NUMBER OF SEQUENCES: 66
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Flanagan, Henderson, Farabow, Garrett &
;; ADDRESSEE: Dunner
;; STREET: 1300 I Street, N.W.
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20005-3315
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/313,185
;; FILING DATE: 12-OCT-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Kenneth J.
;; REGISTRATION NUMBER: 25,146
;; REFERENCE/DOCKET NUMBER: 02356.0068-00000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 408-4000
;; TELEFAX: (202) 408-4400
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3447 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;;
US-08-313-185-57

Query Match 70.0%; Score 14; DB 2; Length 3447;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gtttcgatgaacc 20
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Db 1448 GTTCGATGAMCCC 1435

Search completed: August 7, 2002, 23:51:48
Job time: 7174 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:04:01 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20
Sequence: 1 tacgctgcgcgcgcgcgcgcgc 20

Scoring table: IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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- 11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	17	AAT12092
2	20	100.0	20	21	AAA49823
3	20	100.0	20	21	AAA49825
4	20	100.0	306	19	AAK27214
5	20	100.0	306	19	AAK27175
6	20	100.0	306	19	AAK27179
7	20	100.0	306	19	AAK27180
8	20	100.0	306	24	AAS99526
9	20	100.0	306	24	AAS99527

10	20	100.0	306	24	AAS99530	Mycobacterium spec
11	20	100.0	306	24	AAS99531	Mycobacterium spec
12	20	100.0	432	14	AA061457	M. tuberculosis ip
13	20	100.0	480	21	AA449863	Mycobacterium tube
14	20	100.0	970	17	AAT09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAH74651	Mycobacterium tube
18	20	100.0	3853	21	AAH89994	M. tuberculosis ip
19	19	95.0	306	19	AAK27217	Mycobacterium spec
20	19	95.0	306	24	AAS99551	Mycobacterium spec
21	19	95.0	21500	23	AAS59633	Propionibacterium
22	18.4	92.0	25	17	AAT12091	M. tuberculosis ip
23	18.4	92.0	306	19	AAK27218	Rpob gene fragment
24	18.4	92.0	306	19	AAK27193	Rpob gene fragment
25	18.4	92.0	306	19	AAK27196	Rpob gene fragment
26	18.4	92.0	306	19	AAK27177	Rpob gene fragment
27	18.4	92.0	306	19	AAK27182	Rpob gene fragment
28	18.4	92.0	306	19	AAK27183	Rpob gene fragment
29	18.4	92.0	306	24	AAS99539	Mycobacterium spec
30	18.4	92.0	306	24	AAS99557	Mycobacterium spec
31	18.4	92.0	27426	23	AAS59541	Propionibacterium
32	18	90.0	87	22	AAC88922	Mycobacterium tube
33	17.4	87.0	306	19	AAK27212	Rpob gene fragment
34	17.4	87.0	306	19	AAK27216	Rpob gene fragment
35	17.4	87.0	306	19	AAK27219	Rpob gene fragment
36	17.4	87.0	306	19	AAK27220	Rpob gene fragment
37	17.4	87.0	306	19	AAK27198	Rpob gene fragment
38	17.4	87.0	306	19	AAK27204	Rpob gene fragment
39	17.4	87.0	306	19	AAK27186	Rpob gene fragment
40	17.4	87.0	306	19	AAK27189	Rpob gene fragment
41	17.4	87.0	306	24	AAS99534	Mycobacterium spec
42	17.4	87.0	306	24	AAS99543	Mycobacterium spec
43	17.4	87.0	306	24	AAS99560	Mycobacterium spec
44	17.4	87.0	306	24	AAS99565	Mycobacterium spec
45	17.4	87.0	306	24	AAS99568	Mycobacterium spec

ALIGNMENTS

RESULT 1	
ID AAT12092	standard; DNA; 20 BP.
AC AAT12092:	
DT 10-JUL-1996	(first entry)
DE M. tuberculosis rpob gene fragment amplification primer p2.	
KW Antibiotic; resistance; spectrum; gene; mycobacterium;	
KW determination; amplification; tuberculosis; rpob; fragment;	
KW primer; differential; hybridisation; pattern; rifampicin;	
KW rifabutin; species identification; ss.	
OS Synthetic.	
PN W0938851-A20	
PD 14-DEC-1995.	
XX 09-JUN-1995:	95MO-EP02230.
XX 09-JUN-1994:	94BP-0870093.
XX (INNO-) INNOGENETICS NV.	
XX De Beenhouwer H, Jannes G, Machtelinckx L, Portels F;	
XX Kossau R;	
XX WPI; 1996-040250/04.	

PT Probes and primers for determin. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determin.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgctacc 20
|||||
DB 1 tacggtcgcgcgagctgctacc 20

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgctacc 20
|||||
DB 1 tacggtcgcgcgagctgctacc 20

RESULT 3

AAAA9825
ID AAA49825 standard; DNA: 20 BP.
XX
AC AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX

PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpob*, *katG*, *rrsL*/512
CC and 235 genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacgctcggcgagctgattcc 20
Db 1 tacgctcggcgagctgattcc 20

RESULT 4

AAx27214
ID AAX27214 standard; DNA; 306 BP.

AAx27214;

27-MAY-1999 (first entry)

RpoB gene fragment.

RpoB gene: *mycobacteria*; phylogenetic tree construction;
KW *mycobacterial* species identification; phylogenetic analysis; ss.

XX *Mycobacteria tuberculosis*.

XX W09905316-A1.

04-FEB-1999.

28-JUL-1998; 98KR-0000228.

28-JUL-1997; 97KR-0035501.

(BION-) BIONEER CORP.

Kim B, Kook Y;

WPI; 1998-539367/46.

XX New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *rpob* gene from *mycobacterial*
PT species, useful for detecting and identifying *mycobacterial* species
XX Claim 43; Page 75-76; 91pp; English.

CC This sequence represents a *mycobacterial* *rpob* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying *mycobacterial* species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpob* gene (encoding the beta
CC subunit of RNA polymerase) from *mycobacterial* species provides an
CC efficient way of characterizing these species. In addition to
CC phylogenetic analysis, the *rpob* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable *mycobacteria*. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.

XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacgctcggcgagctgattcc 20
Db 5 tacgctcggcgagctgattcc 24

RESULT 5

AAx27175
ID AAX27175 standard; DNA; 306 BP.

AAx27175;

27-MAY-1999 (first entry)

RpoB gene fragment.

RpoB gene: *mycobacteria*; phylogenetic tree construction;
KW *mycobacterial* species identification; phylogenetic analysis; ss.

XX *Mycobacteria africanum*.

XX W09905316-A1.

04-FEB-1999.

28-JUL-1998; 98KR-0000228.

28-JUL-1997; 97KR-0035501.

(BION-) BIONEER CORP.

Kim B, Kook Y;

WPI; 1998-539367/46.

XX New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *rpob* gene from *mycobacterial*
PT species, useful for detecting and identifying *mycobacterial* species
XX Claim 4; Page 62-63; 91pp; English.

CC This sequence represents a *mycobacterial* *rpob* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying *mycobacterial* species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpob* gene (encoding the beta
CC subunit of RNA polymerase) from *mycobacterial* species provides an
CC efficient way of characterizing these species. In addition to
CC phylogenetic analysis, the *rpob* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable *mycobacteria*. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.

XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacgctcggcgagctgattcc 20
Db 5 tacgctcggcgagctgattcc 24

RESULT 6

AAx27179

```
ID AAX27179 standard; DNA; 306 BP.
XX
XX AAX27179;
AC
XX
XX
DT 27-MAY-1999 (first entry)
DE
XX RpoB gene fragment.
XX
XX RpoB gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
XX Mycobacteria bovis.
OS
XX
XX WO905316-A1.
XX
XX 04-FEB-1999.
XX
XX
XX PF 28-JUL-1998; 98KR-0000228.
XX
XX PR 28-JUL-1997; 97KR-0035501.
XX
XX (BION-) BIONEER CORP.
XX
XX Kim B, Kook Y;
PI
XX
XX WPI; 1998-539367/46.
XX
XX
XX PT New pair of polymerase chain reaction (PCR) primers - for
XX sequence-specific amplification of the rpoB gene from mycobacterial
XX species, useful for detecting and identifying mycobacterial species
XX
XX Claim 8; Page 64; 91pp; English.
XX
XX This sequence represents a mycobacterial rpoB gene fragment, that is
XX amplified using the PCR primers of the invention. The primers form a
XX method of detecting and identifying mycobacterial species by constructing
XX a phylogenetic tree for the species. The use of the primers for
XX sequence-specific amplification of the rpoB gene (encoding the beta
XX subunit of RNA polymerase) from mycobacterial species provides an
XX efficient way of characterizing these species. In addition to
XX phylogenetic analysis, the rpoB gene can be used as an alternative to
XX the 16S rRNA gene because it has four subunits, which are highly
XX conserved throughout prokaryotes. The method is particularly useful for
XX slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
XX susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 19; Length 306;
XX Best Local Similarity 100.0%; Pred. No. 1.6;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tagcgtcgcgagctgattcc 20
XX |||||||||||||||||||
XX Db 5 tagcgtcgcgagctgattcc 24
XX
XX
XX RESULT 7
XX AAX27180
XX ID AAX27180 standard; DNA; 306 BP.
XX
XX AAX27180;
AC
XX
XX 27-MAY-1999 (first entry)
DE
XX RpoB gene fragment.
XX
XX RpoB gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
XX Mycobacteria bovis.
XX
```

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PN WO905316-A1.
XX
XX 04-FEB-1999.
XX
XX
XX PF 28-JUL-1998; 98KR-0000228.
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XX PR 28-JUL-1997; 97KR-0035501.
XX
XX (BION-) BIONEER CORP.
XX
XX Kim B, Kook Y;
PI
XX
XX WPI; 1998-539367/46.
XX
XX
XX PT New pair of polymerase chain reaction (PCR) primers - for
XX sequence-specific amplification of the rpoB gene from mycobacterial
XX species, useful for detecting and identifying mycobacterial species
XX
XX Claim 9; Page 64; 91pp; English.
XX
XX This sequence represents a mycobacterial rpoB gene fragment, that is
XX amplified using the PCR primers of the invention. The primers form a
XX method of detecting and identifying mycobacterial species by constructing
XX a phylogenetic tree for the species. The use of the primers for
XX sequence-specific amplification of the rpoB gene (encoding the beta
XX subunit of RNA polymerase) from mycobacterial species provides an
XX efficient way of characterizing these species. In addition to
XX phylogenetic analysis, the rpoB gene can be used as an alternative to
XX the 16S rRNA gene because it has four subunits, which are highly
XX conserved throughout prokaryotes. The method is particularly useful for
XX slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
XX susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
XX
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XX Query Match 100.0%; Score 20; DB 19; Length 306;
XX Best Local Similarity 100.0%; Pred. No. 1.6;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 tagcgtcgcgagctgattcc 20
XX |||||||||||||||||||
XX Db 5 tagcgtcgcgagctgattcc 24
XX
XX
XX RESULT 8
XX AAS99526
XX ID AAS99526 standard; DNA; 306 BP.
XX
XX AAS99526;
AC
XX
XX 12-MAR-2002 (first entry)
DE
XX Mycobacterium tuberculosis.
XX
XX Drug resistance detection; mycobacterial species identification; probe;
XX oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
XX primer.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200192573-A1.
XX
XX 06-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-KR00904.
XX
XX 30-MAY-2000; 2000KR-0029369.
XX
XX (BION-) BIOMEDLAB CO LTD.
XX
XX Kim H, Kim N, Yoon S, Kim J, Park M;
XX
```

DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PS probe -
XX
XX Disclosure; Page 21; 74pp; English.
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgattcc 20
Db 5 tacggtcgcgcgagctgattcc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA: 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KM Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KM primer.
XX
OS Mycobacterium africanum.
XX
XX WO200192573-A1.
XX
PN 06-DEC-2001.
XX
PD 30-MAY-2001; 2001WO-KR00904.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PS probe -
XX
XX Disclosure; Page 21; 74pp; English.

XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgattcc 20
Db 5 tacggtcgcgcgagctgattcc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA: 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KM Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KM primer.
XX
OS Mycobacterium bovis.
XX
XX WO200192573-A1.
XX
PN 06-DEC-2001.
XX
PD 30-MAY-2001; 2001WO-KR00904.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PS probe -
XX
XX Disclosure; Page 21; 74pp; English.
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS9478-AAS9569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgattcc 20
|||||
DB 5 tacggtcgcgcgagctgattcc 24

RESULT 11

AAS99531
ID AAS99531 standard; DNA; 306 BP.

AC AAS99531;

DT 12-MAR-2002 (first entry)

DE Mycobacterium species identification primer #6.

KM Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;

OS Mycobacterium bovis.

PN WO200192573-A1.

PD 06-DEC-2001.

PF 30-MAY-2001; 2001WO-KR00904.

PR 30-MAY-2000; 2000KR-0029369.

PA (BIOM-) BIOMEDLAB CO LTD.

PI Kim H, Kim N, Yoon S, Kim J, Park M;

DR WPI; 2002-075472/10.

PT Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -

PS Disclosure; Page 21; 74pp; English.

XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS9478-AAS9569
CC represent mycobacterium species identification probes and primers of the
CC invention.

XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgattcc 20
|||||
DB 5 tacggtcgcgcgagctgattcc 24

RESULT 12

AA061457
ID AA061457 standard; DNA; 432 BP.

AC AA061457;

DT 17-MAY-1994 (first entry)

DE M. tuberculosis rpoB gene fragment.

KM rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.

OS Mycobacterium tuberculosis.

PN WO9322454-A.

PD 11-NOV-1993.

PF 30-APR-1993; 93WO-EP01063.

PR 17-SEP-1992; 92FR-0011098.

PR 30-APR-1992; 92US-0875940.

PR 14-AUG-1992; 92US-0929206.

PR 16-APR-1993; 93FR-0004545.

PA (ASSI-) ASSISTANCE PUBLIQUE.

PA (INSP) INST PASTEUR.

PA (MED-) MEDICAL RES COUNCIL.

PA (UYBE-) UNITV BERN.

PA (UYPA-) UNITV CURIE PARIS VI P & M.

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;

PI Young D, Zhang Y;

DR WPI; 1993-368812/46.

DR P-PSDB; AAR51372.

XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium lepreae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M. tuberculosis (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.

SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgagctgattcc 20

```
Db 18 tacggtcgcgcgactgatcc 37
|||||
RESULT 13
AAAA9863
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
Key Location/Qualifiers
FH primer_bind complement(41..60)
FT /tag= a
FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample.
XX
PS Disclosure: Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;
Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 41 tacggtcgcgcgactgatcc 60
|||||
RESULT 14
AAT09676
ID AAT09676 standard; DNA; 970 BP.
XX
AC AAT09676;
XX
DT 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KW polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Mycobacterium tuberculosis.
XX
Key Location/Qualifiers
FH primer_bind 10..27
FT /tag= a
FT /note= "primer FENLEF"
FT primer_bind 226..243
FT /tag= b
FT /note= "primer DDIDHL"
FT primer_bind 226..240
FT /tag= c
FT /note= "primer DDIDH"
FT primer_bind 338..364
FT /tag= d
FT /note= "primer rpo95"
FT primer_bind 348..373
FT /tag= e
FT /note= "primer rpo105"
FT primer_bind 354..373
FT /tag= f
FT /note= "primer KY290"
FT primer_bind 372..373
FT /tag= g
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 433..434
FT /tag= h
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 438
FT /tag= i
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 468..469
FT /tag= j
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 486
FT /tag= k
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 501
FT /tag= l
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 516
FT /tag= m
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 516..535
FT /tag= n
FT /note= "primer rpo273"
FT primer_bind 525
FT /tag= o
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 525..541
FT /tag= p
FT /note= "primer KY292"
FT primer_bind 536..562
FT /tag= q
FT /note= "primer rpo293"
FT primer_bind 640..666
FT /tag= r
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Tt	/note= "primer rpo397"
Ft	primer_bind
Ft	952..966
Ft	/*tag= S
Ft	/note= "primer NMQRQ-1"
Ft	952..966
Ft	/*tag= t
Ft	/note= "primer NMQRQ-2"
Xx	
Xn	
Pd	WO9533074-A1.
Pd	07-DEC-1995.
Pf	
Pf	26-MAY-1995; 95WO-US06790.
Px	
Px	26-MAY-1994; 94US-0250030.
Pa	(HOEF) HOFFMANN LA ROCHE INC.
Pa	(MAYO-) MAYO FOUNDATION.
Pi	
Pi	Rejmbe TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
Pi	Young KKY;
Dk	
Dk	WPI: 1996-030581/03.
Pt	
Pt	Detection of Mycobacterium tuberculosis - by amplifying sample DNA
Pt	with a primer set that targets portions of the gene encoding rpoB.
Xx	
Xx	Disclosure; Fig.3; 54pp; English.
Px	
Cc	This oligonucleotide DNA primer is specific for Mycobacterium
Cc	tuberculosis, and may be used to amplify a sample DNA by targeting
Cc	a portion of the gene encoding rpoB The 1st several bases comprise a
Cc	nonhybridizing tail consisting of filler bases followed by
Cc	a restriction site incorporated to facilitate cloning using the
Cc	amplicon at a later date, if desired. The remaining bases hybridize
Cc	to bacterial rpoB DNA. The method provides for the detection of M.
Cc	tuberculosis and the concurrent determination of its drug
Cc	susceptibility, particularly to rifamycin. The method can provide
Cc	often greater than 95% sensitivity and 100% specificity. The
Cc	biological sample is a fluid or tissue sample from a human.
Sq	
Sq	Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;

Query Match	100.0%	Score 20;	DB 17;	Length 970;
Best Local Similarity	100.0%	Pred. No. 1 6;		
Matches	20;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	tacggtcgcgcagctgattcc	20	
Db	261	tacggtcgcgcagctgattcc	280	

	RESULT	15
AAH51976		
ID	AAH51976	standard; DNA: 3519 BP.
XX		
AC	AAH51976;	
XX		
DT	04-SEP-2001	(first entry)
XX		
DE	Mycobacterium tuberculosis	potential drug target gene SEQ ID 30
XX		
KM	Drug target; growth; organism	viability; characterisation: ds.
XX		
OS	Mycobacterium tuberculosis.	
XX		
PN	W0200135317-A1.	
XX		
PD	17-MAY-2001.	
XX		
PF	13-NOV-2000; 2000WO-US31152.	
XX		

12-NOV-1999: 99US-0165086.
12-NOV-1999: 99US-0165124.
01-FEB-2000: 2000US-0179531.
(REGC) UNIV CALIFORNIA.
Eisenberg D, Rotstein SH, Marcotte EM;
WPI: 2001-329193/34.
P-PSDB; AAG81125.
Identifying nucleotide or polypeptide sequence for use as drug target,
involves providing algorithm that analyzes a functional relationship
between nucleotide or polypeptide sequences, and comparing the
sequences -
Disclosure: Page 68-69; 207pp; English.

	Query Match	100.0%	Score 20;	Length 3519;
	Best Local Similarity	100.0%;	Pred. No. 1.6;	
	Matches	20;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0
OY	1 tacggtcgcgcagctgatcc	20		
DB	1119 tacggtcgcgcagctgatcc	1138		

Search completed: August 7, 2002, 22:04:01
Job time: 8061 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 19:49:40 ; Search time 568.44 Seconds

(Without alignments)
60,408 Million cell updates/sec

Title: US-09-786-105-1

Sequence: 1 tacgctgcgcgcgcgcgcgc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	17	AA112092
2	20	100.0	20	21	AAA49823
3	20	100.0	20	21	AAA49825
4	20	100.0	306	19	AAx27214
5	20	100.0	306	19	AAx27175
6	20	100.0	306	19	AAx27179
7	20	100.0	306	19	AAx27180
8	20	100.0	306	24	AAx27180
9	20	100.0	306	24	AAx27180

10	20	100.0	306	24	AAx27180	Mycobacterium spec
11	20	100.0	306	24	AAx27180	Mycobacterium spec
12	20	100.0	432	14	AAx27180	Mycobacterium spec
13	20	100.0	480	21	AAx27180	Mycobacterium spec
14	20	100.0	970	17	AAx27180	Mycobacterium spec
15	20	100.0	3519	22	AAx27180	Mycobacterium spec
16	20	100.0	3534	22	AAx27180	Mycobacterium spec
17	20	100.0	3853	21	AAx27180	Mycobacterium spec
18	20	100.0	3853	21	AAx27180	Mycobacterium spec
19	20	100.0	3853	21	AAx27180	Mycobacterium spec
20	20	100.0	3853	21	AAx27180	Mycobacterium spec
21	20	100.0	3853	21	AAx27180	Mycobacterium spec
22	20	100.0	3853	21	AAx27180	Mycobacterium spec
23	20	100.0	3853	21	AAx27180	Mycobacterium spec
24	20	100.0	3853	21	AAx27180	Mycobacterium spec
25	20	100.0	3853	21	AAx27180	Mycobacterium spec
26	20	100.0	3853	21	AAx27180	Mycobacterium spec
27	20	100.0	3853	21	AAx27180	Mycobacterium spec
28	20	100.0	3853	21	AAx27180	Mycobacterium spec
29	20	100.0	3853	21	AAx27180	Mycobacterium spec
30	20	100.0	3853	21	AAx27180	Mycobacterium spec
31	20	100.0	3853	21	AAx27180	Mycobacterium spec
32	20	100.0	3853	21	AAx27180	Mycobacterium spec
33	20	100.0	3853	21	AAx27180	Mycobacterium spec
34	20	100.0	3853	21	AAx27180	Mycobacterium spec
35	20	100.0	3853	21	AAx27180	Mycobacterium spec
36	20	100.0	3853	21	AAx27180	Mycobacterium spec
37	20	100.0	3853	21	AAx27180	Mycobacterium spec
38	20	100.0	3853	21	AAx27180	Mycobacterium spec
39	20	100.0	3853	21	AAx27180	Mycobacterium spec
40	20	100.0	3853	21	AAx27180	Mycobacterium spec
41	20	100.0	3853	21	AAx27180	Mycobacterium spec
42	20	100.0	3853	21	AAx27180	Mycobacterium spec
43	20	100.0	3853	21	AAx27180	Mycobacterium spec
44	20	100.0	3853	21	AAx27180	Mycobacterium spec
45	20	100.0	3853	21	AAx27180	Mycobacterium spec

ALIGNMENTS

RESULT 1

AA112092

ID AA112092 standard; DNA: 20 BP.

XX

XX AA112092:

XX

XX 10-JUL-1996 (first entry)

XX

XX M. tuberculosis rpoB gene fragment amplification primer P2.

XX

XX Antibiotic resistance: spectrum; gene; mycobacterium;

XX determination: amplification; tuberculosis; rpoB; fragment;

XX primer; differential; hybridisation; pattern; rifampicin;

XX rifabutin; species identification; ss.

XX

XX Synthetic.

XX

XX W0383851-A2.

XX

XX 14-DEC-1995.

XX

XX 09-JUN-1995; 95NO-EP02230.

XX

XX 09-JUN-1994; 94EP-0870093.

XX

XX (INNO-) INNOGENETICS NV.

XX

XX De Beenhouwer H, Jannes G, Machteldinckx L, Portaeis F,

XX Kossau R;

XX

XX WPI: 1996-040250/04.

XX

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS and opt. the spp. from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgatcc 20
|||||
Db 1 tacggtcgcgcgagctgatcc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.

AC AAA49823;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgatcc 20
|||||
Db 1 tacggtcgcgcgagctgatcc 20

RESULT 3

AAA49825
ID AAA49825 standard; DNA; 20 BP.

AC AAA49825;

DT 25-SEP-2000 (first entry)

DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

OS Mycobacterium tuberculosis.

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI: 2000-431611/37.

PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgacc 20
|||||
DB 1 tacgctcgagcagctgacc 20

RESULT 4
AAx27214
ID AAX27214 standard; DNA: 306 BP.
XX
XX AAX27214;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KM RpoB gene: mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria tuberculosis.
XX
PN W09905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 43; Page 75-76; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgacc 20
|||||
DB 5 tacgctcgagcagctgacc 24

RESULT 5
AAX27175
ID AAX27175 standard; DNA: 306 BP.
XX
XX AAX27175;
XX
DT 27-MAY-1999 (first entry)
XX
DE RpoB gene fragment.
XX
KM RpoB gene: mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
OS Mycobacteria africanum.
XX
PN W09905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 4; Page 62-63; 91pp; English.
XX
CC This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgacc 20
|||||
DB 5 tacgctcgagcagctgacc 24

RESULT 6
AAX27179

```

ID  AAX27179 standard; DNA; 306 BP.
XX
XX  AAX27179:
AC
XX
XX  27-MAY-1999 (first entry)
DT
XX
XX  RPOB gene fragment.
DE
XX
XX  RPOB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
XX  Mycobacteria bovis.
OS
XX
XX  WO9905316-A1.
PN
XX
XX  04-FEB-1999.
PD
XX
XX  28-JUL-1998; 98KR-0000228.
PF
XX
XX  28-JUL-1997; 97KR-0035501.
PR
XX
XX  (BION-) BIONEER CORP.
PA
XX
XX  Kim B, Kook Y;
PI
XX
XX  WPI; 1998-539367/46.
DR
XX
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PR  species, useful for detecting and identifying mycobacterial species
PS  Claim 8; Page 64; 91pp; English.

CC  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterizing these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX  Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
SQ

Query Match          100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 tacggtcgcgagctgaccc 20
    |||
Db  5 tacggtcgcgagctgaccc 24

RESULT 7
AAX27180
ID  AAX27180 standard; DNA; 306 BP.
XX
XX  AAX27180:
AC
XX
XX  27-MAY-1999 (first entry)
DT
XX
XX  RPOB gene fragment.
DE
XX
XX  RPOB gene; mycobacteria; phylogenetic tree construction;
KM  mycobacterial species identification; phylogenetic analysis; ss.
XX
XX  Mycobacteria bovis.
OS
XX

```

```

PN  WO9905316-A1.
XX
XX  04-FEB-1999.
PD
XX
XX  28-JUL-1998; 98KR-0000228.
PF
XX
XX  28-JUL-1997; 97KR-0035501.
PR
XX
XX  (BION-) BIONEER CORP.
PA
XX
XX  Kim B, Kook Y;
PI
XX
XX  WPI; 1998-539367/46.
DR
XX
XX  New pair of polymerase chain reaction (PCR) primers - for
PT  sequence-specific amplification of the rpoB gene from mycobacterial
PR  species, useful for detecting and identifying mycobacterial species
PS  Claim 9; Page 64; 91pp; English.

CC  This sequence represents a mycobacterial rpoB gene fragment, that is
CC  amplified using the PCR primers of the invention. The primers form a
CC  method of detecting and identifying mycobacterial species by constructing
CC  a phylogenetic tree for the species. The use of the primers for
CC  sequence-specific amplification of the rpoB gene (encoding the beta
CC  subunit of RNA polymerase) from mycobacterial species provides an
CC  efficient way of characterizing these species. In addition to
CC  phylogenetic analysis, the rpoB gene can be used as an alternative to
CC  the 16S rRNA gene because it has four subunits, which are highly
CC  conserved throughout prokaryotes. The method is particularly useful for
CC  slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC  susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX  Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ

Query Match          100.0%; Score 20; DB 19; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 tacggtcgcgagctgaccc 20
    |||
Db  5 tacggtcgcgagctgaccc 24

RESULT 8
AAS99526
ID  AAS99526 standard; DNA; 306 BP.
XX
XX  AAS99526:
AC
XX
XX  12-MAR-2002 (first entry)
DT
XX
XX  Mycobacterium species identification primer #1.
DE
XX
XX  Mycobacterium tuberculosis.
OS
XX
XX  Drug resistance detection; mycobacterial species identification; probe;
KM  oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW  primer.
XX
XX  Mycobacterium tuberculosis.
OS
XX
XX  WO200192573-A1.
PN
XX
XX  06-DEC-2001.
PD
XX
XX  30-MAY-2001; 2001WO-KR00904.
PF
XX
XX  30-MAY-2000; 2000KR-0029369.
PR
XX
XX  (BION-) BIOMEDLAB CO LTD.
PA
XX
XX  Kim H, Kim N, Yoon S, Kim J, Park M;
PI
XX

```

DR WPI; 2002-075472/10.
XX
XX Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
XX Disclosure; Page 21; 74pp; English.
XX
CC The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgcgcgagctgaccc 20
Db 5 tacggtcgcgcgagctgaccc 24
XX
XX
XX RESULT 9
AAS99527
ID AAS99527 standard; DNA: 306 BP.
XX
XX AAS99527;
XX
XX 12-MAR-2002 (first entry)
XX
XX Mycobacterium species identification primer #2.
XX
XX Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
XX Mycobacterium africanum.
OS
XX WO200192573-A1.
PN
XX 06-DEC-2001.
PD
XX 30-MAY-2001; 2001WO-KR00904.
PF
XX 30-MAY-2000; 2000KR-0029369.
PR
XX (BIOM-) BIOMEDLAB CO LTD.
PA
XX Kim H, Kim N, Yoon S, Kim J, Park M;
PI WPI; 2002-075472/10.
XX
XX
XX Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
XX Disclosure; Page 21; 74pp; English.

XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggtcgcgcgagctgaccc 20
Db 5 tacggtcgcgcgagctgaccc 24
XX
XX
XX RESULT 10
AAS99530
ID AAS99530 standard; DNA: 306 BP.
XX
XX AAS99530;
XX
XX 12-MAR-2002 (first entry)
XX
XX Mycobacterium species identification primer #5.
XX
XX Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
XX Mycobacterium bovis.
OS
XX WO200192573-A1.
PN
XX 06-DEC-2001.
PD
XX 30-MAY-2001; 2001WO-KR00904.
PF
XX 30-MAY-2000; 2000KR-0029369.
PR
XX (BIOM-) BIOMEDLAB CO LTD.
PA
XX Kim H, Kim N, Yoon S, Kim J, Park M;
PI WPI; 2002-075472/10.
XX
XX
XX Kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
PT probe -
XX
XX Disclosure; Page 21; 74pp; English.
XX
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of

CC	mycobacterial rpoB gene and the detection probe is comprised of one or
CC	more modified codons of mycobacterial rpoB gene. The method involves
CC	amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC	(PCR) and discriminating species by fluorescent intensity corresponding
CC	to a particular species. The specimen is preferably uncultured sputum,
CC	blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC	represent mycobacterium species identification probes and primers of the
CC	invention.
SQ	Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
XX	
Query Match	100.0%; Score 20; DB 24; Length 306;
Best Local Similarity	100.0%; Pred. No. 1.6;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 taaggtcgcgagactgatcc 20
DB	5 tacgctgcgcgagctcatcc 24
RESULT 11	
AAS99531	
ID	AAS99531 standard; DNA; 306 BP.
XX	
AC	AAS99531;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Mycobacterium species identification primer #6.
XX	
KW	Drug resistance detection; mycobacterial species identification; probe;
KM	oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW	primer.
XX	
OS	Mycobacterium bovis.
XX	
PN	WO200192573-A1.
PD	06-DEC-2001.
PF	30-MAY-2001; 2001WO-KR00904.
PR	30-MAY-2000; 2000KR-0029369.
PA	(BIOM-) BIOMEDLAB CO LTD.
PI	Kim H, Kim N, Yoon S, Kim J, Park M;
DR	WPI; 2002-075472/10.
PT	
PT	Kit for mycobacterial species identification and drug resistance
PT	detection, has oligonucleotide chip with species identification probe,
PT	a mycobacterial drug-resistance detection probe, and its contrast group
PT	probe -
PS	
PS	Disclosure: Page 21; 74pp; English.
XX	
XX	The invention relates to a diagnostic kit for mycobacterial species
CC	identification and drug resistance detection comprising an
CC	oligonucleotide chip including a species identification probe, a
CC	mycobacterial drug-resistance detection probe, a contrast group probe
CC	corresponding to each drug resistance detection probe, and a marker for
CC	detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC	identification probe is comprised of species-specific DNA sequences of
CC	mycobacterial rpoB gene and the detection probe is comprised of one or
CC	more modified codons of mycobacterial rpoB gene. The method involves
CC	amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC	(PCR) and discriminating species by fluorescent intensity corresponding
CC	to a particular species. The specimen is preferably uncultured sputum,
CC	blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC	represent mycobacterium species identification probes and primers of the
CC	invention.

```

XX      SQ      Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
Query Match          100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. NO. 1.6;
Matches    20; Conservative   0; Mismatches    0; Indels     0; Gaps     0
OY      1 tacggtcgcgcagctgatcc 20
        |||
Db       5 tacggtcgcgcagctgatcc 24
RESULT 12
AA061457
ID      AA061457 standard; DNA; 432 BP.
AC      AA061457;
AT      17-MAY-1994 (first entry)
DE      M.tuberculosis rpoB gene fragment.
KW      rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
OS      mutant; ss.
PN      Mycobacterium tuberculosis.
PD      WO9322454-A.
PI      11-NOV-1993.
PF      30-APR-1993; 93WO-EP01063.
PR      17-SEP-1992; 92FR-0011098.
PR      30-APR-1992; 92US-0875940.
PR      14-AUG-1992; 92US-0929206.
PR      16-APR-1993; 93FR-0004545.
PA      (ASSI-) ASSISTANCE PUBLIQUE.
PA      (INSP) INST PASTEUR.
PA      (MEDI-) MEDICAL RES COUNCIL.
PA      (UYBE-) UNIV BERNE.
PA      (UYRA-) UNIV CURIE PARIS VI P & M.
XX      Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI      Young D, Zhang Y;
XX      WPI: 1993-368812/46.
DR      P-PsDB; AMR51372.
XX      Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT      isoloniaid, rifampicin or streptomycin resistance in tuberculosis
PT      by detecting mutation in katG, rpoB or rpsL genes
XX      Example 2; Fig 13; 97pp; English.
PS      PCR amplification was used to obtain rpoB genes from rifampicin-
CC      resistant Mycobacterium leprae strains. A comparison with the
CC      sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC      mutations in the region encoding amino acids 400-450. The corresp.
CC      region was isolated from M.tuberculosis (AA061457). A common
CC      mutation seen in resistant strains occurs at codon 425 where Ser is
CC      substituted, most frequently by Leu.
SQ      Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;
Query Match          100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. NO. 1.6;
Matches    20; Conservative   0; Mismatches    0; Indels     0; Gaps     0;
OY      1 tacggtcgcgcagctgatcc 20

```


Db 18 tacggtcgcgcgcgtcatcc 37

|||||

```
RESULT 13
AAA49863
ID AAA49863 standard; DNA: 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FH primer_bind complement(41..60)
FT /tag= a
FT /note= "primer of AAA49823"
FT primer_bind 372..391
FT /tag= b
FT /note= "primer of AAA49824"
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PE 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VIST-) VISIBLE GENETICS INC.
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample.
XX
PS Disclosure: Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), gyrA
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (chloramphenicol) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SO Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;
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Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgcgcgtcatcc 20
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Db 41 tacggtcgcgcgcgtcatcc 60

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RESULT 14
AAT09676
ID AAT09676 standard; DNA: 970 BP.
XX
AC AAT09676;
XX
DT 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KM Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FH primer_bind 10..27
FT /tag= a
FT /note= "primer FENLFF"
FT primer_bind 226..243
FT /tag= b
FT /note= "primer DDIDHL"
FT primer_bind 226..240
FT /tag= c
FT /note= "primer DDIDH"
FT primer_bind 338..364
FT /tag= d
FT /note= "primer rpo95"
FT primer_bind 348..373
FT /tag= e
FT /note= "primer rpo105"
FT primer_bind 354..373
FT /tag= f
FT /note= "primer KY290"
FT misc_feature 372..373
FT /tag= g
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 433..434
FT /tag= h
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 438
FT /tag= i
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 468..469
FT /tag= j
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 486
FT /tag= k
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 501
FT /tag= l
FT /note= "M. tuberculosis signature nucleotide"
FT misc_feature 516
FT /tag= m
FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 516..535
FT /tag= n
FT /note= "primer rpo273"
FT misc_feature 525
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FT /note= "M. tuberculosis signature nucleotide"
FT primer_bind 525..541
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FT primer_bind 536..562
FT /tag= q
FT /note= "primer rpo293"
FT primer_bind 640..666
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QY 1 tacggtcgagcagctgaccc 20 					
Db 261 tacggtcgagcagctgaccc 280					
RESULT 15					
AAH51976					
ID AAH51976 standard; DNA: 3519 BP.					
AAH51976;					
04-SEP-2001 (first entry)					
Mycobacterium tuberculosis potential drug target gene SEQ ID 30.					
Drug target; growth; organism viability; characterisation; ds.					
Mycobacterium tuberculosis.					
MO200135317-A1.					
17-MAY-2001.					
13-NOV-2000; 2000MO-US31152.					

```

PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
PA (REGC ) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
PI
XX WPI: 2001-329193/34.
DR P-PSDB; AAG81125.
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
PS Disclosure; Page 68-69; 207pp; English.
XX
XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterizing the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 1 tacggtcgcgcagctgatcc 20
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db 1119 tacggtcgcgcagctgatcc 1138

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Search completed: August 7, 2002, 22:03:58
Job time: 8058 sec

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 HTWYKGVSRIGYLLDLAPKDLKTIYFAAVVITSVDEMRHNL"
 BASE COUNT 969 a 1534 c 1691 g 890 t
 ORIGIN
 Query Match 100.0%; Score 20; DB 1; Length 5084;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 tacggcgatttcgattgaacc 20
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 Db 2611 TACGGCGATTTCGATGACCC 2592
 RESULT 15 AE006964 19352 bp DNA linear BCT 27-APR-2001
 AE006964/c LOCUS Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
 DEFINITION complete genome.
 ACCESSION AE006964 AE000516
 VERSION AE006964.1 GI:13880217
 KEYWORDS Mycobacterium tuberculosis CDC1551.
 ORGANISM Mycobacterium tuberculosis CDC1551.
 Bacteria: Firmicutes; Actinobacteriia; Actinobacteridae;
 Actinomycetales; Corynebacteriales; Mycobacteriaceae;
 Mycobacterium; Mycobacterium tuberculosis complex.
 REFERENCE 1 (bases 1 to 19352)
 AUTHORS Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
 Peterson, J.F., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
 Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
 Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
 Gill, J., Mikula, A. and Bishai, W.
 TITLE Whole genome comparison of Mycobacterium tuberculosis clinical and
 laboratory strains
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 19352)
 AUTHORS Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
 Peterson, J.F., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
 Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
 Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H.,
 Gill, J., Mikula, A. and Bishai, W.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712
 Medical Center Dr, Rockville, MD 20850, USA
 FEATURES
 SOURCE Location/Organism
 1. 19352
 /organism="Mycobacterium tuberculosis CDC1551"
 /strain="CDC1551"
 /db_xref="taxon:83331"
 /note="clinical strain"
 163. 3699
 /gene="MT0695"
 163. 3699
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 /note="similar to GB:L27989 GB:L05910 GB:U12205 SP:P47766
 P1D:149992. Identified by sequence similarity; putative"
 /codon_start=1
 /transl_table=1
 /product="DNA-directed RNA polymerase, beta subunit"
 /protein_id="AAK44921.1"
 /db_xref="GI:13880218"
 /translation="MLGCGTILADRSKSTASPSRROSSNNNSVGPAPRVAPAKL
 REPLEVPEGLDVQDTSFEMLTGSPRMSAERGDVNPVGLIEVLELSPIDEPSS
 MSLSFSDPRFDVAPVDECKDKMTYAAPLEVAEPLNNNGEIKSGVTMGDPMM
 TEKCTFIPRTERVAVSOLVRSVGVYEDETIDKSTDKTSHSVKVIIPSGAVLEFDVAK
 RDVAVRDRKRPQVTVLTKALGWTSEQIVERTGSEIRMSSTLEKNDVTGDEALD
 IYRLRGEPEPTKSAOTLLENLFKEKRYDLARVGRYKVKKLGKLGAVGEPITSSTL
 EEDVATIEVLRLEHGTMTVPGVGEVPEVETDIDHFGNRLRTVELLONDIRG
 MSRMERYVREMTTODVAITPQILINIRPVVAIKFEFTQSLSQFQDNPNPISGLT
 HKRLSLALPGSLSRERAGLEVRDHPHSHYGRMCPETPEGPNIGLIGLSVYKAVNP

FGFIEPIRYKVVGVSDVLYITLADIEDRHVYAQANSPIADAGREPREPVLYRRKAG
 ENEYVMSLEADYDVSPROMVSAITMIPLEDDNNRNLNMGRTNMRQAVPLVRSAP
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 DEDELPAVAVNELVRYVADKRTISDGDKLGRGKNGVIGKILIPVDMPELADGPEVD
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 SPVFDGAQEAELAGLISCTLPNRDGVLDVADGKAMLPDGRSGEPFPVPTVGVYI
 MKLHLVDDKIHARSTGSPMITQOPLGKAGCGGOFCEGMCAQAVGAATYLOEL
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 similarity; putative"
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 /product="DNA-directed RNA polymerase, beta-prime subunit"
 /protein_id="AAK44922.1"
 /db_xref="GI:13880219"
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 GLTCEKIFGPTROMCEYCGKRYRFRGICERCGEVTRAKYRRERMGHITLAPVT
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 AVEORDGELBAROKLEADLAELEAGAAADARRKVRDGEREMQIRORAEULDR
 LEDIWSFTFKARQOLVDENLYRELDRYGEYFTGMAGAESLOKLENDIDIAEAS
 LRDVIRMGKOKKRLALKRLKVAAPFOOSGNSPMGMAVETLGRVFNELPLIGYR
 PATSDLDLRYVIRNRRNLKRLDGAPELTIYNKEMKPOESVDLFDNGRGPAT
 GPGKRPILKSLDKGKGRFRLNLRKRDVSGRSYIVYGPOKLHQKCLPLMALE
 LKFRPVKRLVLDLNAHONISAKRWERORQVWADVLEVYIAEPVLLQACAPTLHRIG
 IOAFEPMLVEGKAIOLHPILVCEAFNADPDDONAVALPLSAQAQAEARILMLSSNLT
 SPASGRPLMRDLDMVGLYLTETVEDEGEOPASGDPEITGVSSPAEALMAADR
 GVLVSRRAKIVYRQLRPLVEIEAELEFGWOGPDGMAAETTLGRVFNELPLIGYR
 PVKMKHKKYQAAITINDLAREVPIVAVGVNDKDGFMVAPSPGVTVMADVLVPE
 RKKEILDHIEERADKVEKORQALNNDENEALEVYKSSFRGLVILEYFINTHA
 ITIVDSGATNGFTOTRLAGMKGLVTPNGEETLPRVYKSPFRGLVILEYFINTHA
 RKLADPALRTADSGYLTRLVDSOVIVREHDCOTERGIVELARABRAGTLIRDP
 YIETSAAYARTLGTDAVDAGNVIVERCODIDEDIALLAGITQVNRVSLVCANST
 GVCATGYSRMAKTLVDIGAVGIVAAOSIGERGQTLNRTFHGQGVRLIGSLR
 VOELFEARVPRKAPLADVGRVRLDEGEREYKLTIVPDGGEVVDKISKROLRV
 FKHDGSEVRLSDGDHVEVQOQLESGADPHEVIRVNGPREVOIHIVREOVRYRAG
 VSHDKHIEVIRQMLRVTIIDSGSTFELPGSLIDAEBAERKRVVAGSGEPAAR
 PVLNIGITKASLADTSMLSAASFQETTVLTDAINCSDKLNGKLENVITGKLIPACT
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 authentic frameshift"
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 PF01261"
 /codon_start=1
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Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
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Db 1547 TACGGCGTTTCGATGAACCC 1528

RESULT 13
LOCUS MTU12205/c

DEFINITION Mycobacterium tuberculosis H37Rv RNA polymerase beta subunit (rpoB)
gene, partial cds.

ACCESSION U12205
VERSION U12205.1 GI:515684

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

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REFERENCE

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JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Query Match 100.0% Score 20; DB 1; Length 3653;
Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 14
LOCUS MSGRPOB/c

DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
gene, complete cds and RNA polymerase beta-subunit rpoC gene,
partial cds.

ACCESSION L27989.1 GI:468333

VERSION L27989

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

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REFERENCE

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TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

partial cds.
 AF060353
 VERSION AF060353.1 GI:3133464
 KEYWORDS
 SOURCE Mycobacterium tuberculosis.
 ORGANISM Mycobacterium tuberculosis.
 Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium tuberculosis complex.
 1 (bases 1 to 705)
 GINGERAS, T.R., GHANDOUR, G., WANG, E., BERNO, A., SMALL, P.M.,
 DROBNIEWSKI, F., ALLAND, D., DESMOND, E., HOLODILY, M., and DRENKOW, J.
 Simultaneous genotyping and species identification using
 hybridization pattern recognition analysis of generic mycobacterium
 DNA arrays
 JOURNAL Genome Res. 8 (5), 435-448 (1998)
 MEDLINE 98248685
 REFERENCE 2 (bases 1 to 705)
 GINGERAS, T.R., GHANDOUR, G., WANG, E., BERNO, A., SMALL, P.M.,
 DROBNIEWSKI, F., ALLAND, D., DESMOND, E., HOLODILY, M., and DRENKOW, J.
 Direct Submission
 TITLE Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
 380 Central Expressway, Santa Clara, CA 95051, USA
 JOURNAL Location/Qualifiers
 FEATURES
 source 1..705
 /organism="Mycobacterium tuberculosis"
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 /db_xref="GI:3133465"
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 HKRRLSALPGSLSRERAGLEVRDHPHSRGMCPITPGSPNGLIGSLSVARVP
 FGRIETPRKYVGVGCVSDERTVYLTADEDDHVAQAQSPIDADGRFVPEPVYRRKAG
 EGVTPSEVDYNDVSPROMVSATNATIPLEHDDANRALMGANMORAVPLVASEAP
 LVGTGMLRAIADAT"
 BASE COUNT 117 a 227 c 250 g 111 t
 ORIGIN

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OY 1 tacggcgttcgatgaacc 20
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 DB 331 TACGGCGTTTCGATGAACCC 312

RESULT 10
 ARI49128/c 706 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI49128
 DEFINITION Sequence 24 from patent US 6228575.
 ARI49128
 ACCESSION ARI49128
 VERSION ARI49128.1 GI:15113719
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 706)
 GINGERAS, T.R., MACK, D., CHEE, M.S., BERNO, A.J., STYER, L.,
 GHANDOUR, G., and WANG, C.
 TITLE ChIP-based species identification and phenotypic characterization
 of microorganisms
 JOURNAL Patent: US 6228575-A 24 08-MAY-2001;
 FEATURES Location/Qualifiers

source 1..706
 /organism="unknown"
 BASE COUNT 117 a 227 c 250 g 111 t 1 others
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 706;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
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 DB 332 TACGGCGTTTCGATGAACCC 313

RESULT 11
 150706/c 970 bp DNA linear PAT 07-OCT-1997
 LOCUS 150706
 DEFINITION Sequence 1 from patent US 5643723.
 150706
 ACCESSION 150706
 VERSION 150706.1 GI:2472409
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 970)
 PERSING, D.H., HUNT, J.J., YOUNG, K.K.Y., FEJMLIE, T.A., ROBERTS, G.D.,
 and WHELAN, A. Christian.
 TITLE Detection of a genetic locus encoding resistance to rifampin in
 mycobacterial cultures and in clinical specimens
 JOURNAL Patent: US 5643723-A 1 01-JUL-1997;
 FEATURES Location/Qualifiers
 source 1..970
 /organism="unknown"
 BASE COUNT 182 a 302 c 330 g 156 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
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 DB 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
 AX111339/c 3534 bp DNA linear PAT 30-APR-2001
 LOCUS AX111339
 DEFINITION Sequence 2072 from Patent WO0123604.
 AX111339
 ACCESSION AX111339
 VERSION AX111339.1 GI:13927631
 KEYWORDS
 SOURCE Mycobacterium tuberculosis.
 ORGANISM Mycobacterium tuberculosis.
 Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Corynebacterineae; Mycobacteriaceae;
 Mycobacterium tuberculosis complex.
 1 (bases 1 to 3534)
 BERGERON, M.G., BOISSINOT, M., HULETSKY, A., m NARD, C., OUELLETTE, M.,
 PICARD, F.J., and ROY, P.H.
 TITLE Highly conserved genes and their use to generate probes and primers
 for detection of microorganisms
 JOURNAL Patent: WO 0123604-A 2072 05-APR-2001;
 Infectio Diagnostic (I.D.I.) INC. (CA)
 FEATURES Location/Qualifiers
 source 1..3534
 /organism="Mycobacterium tuberculosis"
 /strain="rv"
 /db_xref="taxon:1773"
 BASE COUNT 679 a 1081 c 1188 g 586 t
 ORIGIN

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
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Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c
LOCUS AR062058 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 137 from patent US 5843669.
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
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Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059
LOCUS AR062059 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 138 from patent US 5843669.
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
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Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060
LOCUS AR062060 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 139 from patent US 5843669.
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061
LOCUS AR062061 620 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 140 from patent US 5843669.
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c
LOCUS AF060353 705 bp DNA linear BCT 15-MAY-1998
DEFINITION Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,

CDS
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188 /replace="c"
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Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
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DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
AR067448/c 432 bp DNA linear PAT 29-SEP-1999
LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
ACCESSION AR067448
VERSION AR067448.1 GI:5998670
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN

Sequence 59 from patent US 5851763.
AR067448
GI:5998670
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 432)
Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
Bodmer, T.
Rapid detection of antibiotic resistance in mycobacterium
tuberculosis
Patent: US 5851763-A 59 22-DEC-1998;
Location/Qualifiers
1..432
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77 a 139 c 149 g 67 t

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Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
AR062056/c AR062056 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062056
DEFINITION Sequence 135 from patent US 5843669.
ACCESSION AR062056
VERSION AR062056.1 GI:5989747
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
BASE COUNT
ORIGIN

Unknown.
Unknown.
Unclassified.
1 (bases 1 to 620)
Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methanococcus
jannaschii FBN-1 endonucleases
Patent: US 5843669-A 135 01-DEC-1998;
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
AR062057/c AR062057 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062057
DEFINITION Sequence 136 from patent US 5843669.
ACCESSION AR062057
VERSION AR062057.1 GI:5989748
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

Unknown.
Unknown.
Unclassified.
1 (bases 1 to 620)
Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methanococcus

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:01 ; Search time 2179.67 Seconds

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192.016 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 taagcgcttcgatagaacc 20

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Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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18: em_ln:*
19: em_mn:*
20: em_om:*
21: em_or:*
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28: em_un:*
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32: em_hcg_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description
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C	5	20	100.0	620	6	AR062058	AR062058 Sequence
	6	20	100.0	620	6	AR062059	AR062059 Sequence
	7	20	100.0	620	6	AR062060	AR062060 Sequence
C	8	20	100.0	620	6	AR062061	AR062061 Sequence
C	9	20	100.0	705	1	AR060353	AR060353 Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128 Sequence
C	11	20	100.0	970	6	IS0706	IS0706 Sequence 1
C	12	20	100.0	3534	6	AX111339	AX111339 Sequence
C	13	20	100.0	3853	1	MTU12205	MTU12205 Mycobacteri
C	14	20	100.0	5084	1	MSGRPOB	MSGRPOB Mycobacte
C	15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
C	16	20	100.0	19770	1	MTC1376	MTC1376 Mycobacteri
C	17	17	85.0	3316	1	AF172323	AF172323 Bacillus
C	18	15	75.0	27	6	IS0714	IS0714 Sequence 9
C	19	15	75.0	11843	1	AE008100	AE008100 Agrobacte
C	20	15	75.0	13735	1	AE009134	AE009134 Agrobacte
	21	15	75.0	239050	1	AL596169	AL596169 Listeria
	22	14	70.0	143	3	AF277396	AF277396 Crithidia
	23	14	70.0	409	1	CSBAG228	CSBAG228 Agrobacte
	24	14	70.0	442	8	AF080428	AF080428 Agrobacte
	25	14	70.0	458	8	AF080421	AF080421 Agrobacte
	26	14	70.0	518	1	AF325874	AF325874 Agrobacte
	27	14	70.0	762	1	SHEPNTC	SHEPNTC Agrobacte
	28	14	70.0	791	33	AC048639	AC048639 Giardia
	29	14	70.0	1128	8	AB044172	AB044172 Yersinia
C	30	14	70.0	1194	3	FHEPMDA	FHEPMDA Agrobacte
C	31	14	70.0	1959	8	ATH10B6A	ATH10B6A Agrobacte
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	35	14	70.0	3240	8	SCU06465	SCU06465 Saccharomyc
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	37	14	70.0	3639	10	AF214568	AF214568 Rattus no
	38	14	70.0	4075	10	AF146044	AF146044 Rattus no
	39	14	70.0	4897	3	AF069181	AF069181 Caenorhabdi
	40	14	70.0	6211	3	CEP14A5	CEP14A5 Sequence
	41	14	70.0	6275	6	AX345453	AX345453 Sequence
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	44	14	70.0	9728	6	AX346805	AX346805 Sequence
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ALIGNMENTS

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LOCUS	Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.				
DEFINITION	MSGRIFRNAP				
ACCESSION	L05910.1 GI:149391				
VERSION	RNA polymerase beta-subunit; rifampicin resistance.				
KEYWORDS	Mycobacterium tuberculosis (strain H37) DNA.				
SOURCE	Mycobacterium tuberculosis				
ORGANISM	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.				
REFERENCE	1 (bases 1 to 432)				
AUTHORS	Telenti, A., Imboden, P., Marchesi, F., Lowrie, D., Cole, S. T., Colston, J., Matter, L., Schopfer, K. and Bodmer, T.				
TITLE	Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis				
JOURNAL	Antimicrob. Agents Chemother. 341, 647-650 (1993)				
FEATURES	Location/Qualifiers				
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	/organism="Mycobacterium tuberculosis"				
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:21 ; Search time 146.61 Seconds
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33.508 Million cell updates/sec

Title: US-09-786-105-3

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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	20	100.0	306	4	US-09-147-935A-6
4	20	100.0	306	4	US-09-147-935A-7
5	20	100.0	306	4	US-09-147-935A-41
6	20	100.0	306	4	US-09-147-935A-50
7	20	100.0	432	2	US-08-313-185-59
8	20	100.0	432	3	US-09-082-614A-59
9	20	100.0	970	1	US-08-250-030-1
10	20	100.0	970	5	PCT-US95-06790-1
11	19	95.0	306	4	US-09-147-935A-44
12	18.4	92.0	25	4	US-08-750-088A-30
13	18.4	92.0	306	4	US-09-147-935A-4
14	18.4	92.0	306	4	US-09-147-935A-9
15	18.4	92.0	306	4	US-09-147-935A-10
16	18.4	92.0	306	4	US-09-147-935A-20
17	18.4	92.0	306	4	US-09-147-935A-23
18	18.4	92.0	306	4	US-09-147-935A-45
19	17.4	87.0	306	4	US-09-147-935A-13
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22	17.4	87.0	306	4	US-09-147-935A-31
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25	17.4	87.0	306	4	US-09-147-935A-46
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28	16.8	84.0	306	4	US-09-147-935A-8	Sequence 8, Appl
29	15.8	79.0	306	4	US-09-147-935A-5	Sequence 5, Appl
30	15.8	79.0	306	4	US-09-147-935A-12	Sequence 12, Appl
31	15.8	79.0	306	4	US-09-147-935A-14	Sequence 14, Appl
32	15.8	79.0	306	4	US-09-147-935A-15	Sequence 15, Appl
33	15.8	79.0	306	4	US-09-147-935A-17	Sequence 17, Appl
34	15.8	79.0	306	4	US-09-147-935A-18	Sequence 18, Appl
35	15.8	79.0	306	4	US-09-147-935A-19	Sequence 19, Appl
36	15.8	79.0	306	4	US-09-147-935A-21	Sequence 21, Appl
37	15.8	79.0	306	4	US-09-147-935A-24	Sequence 24, Appl
38	15.8	79.0	306	4	US-09-147-935A-26	Sequence 26, Appl
39	15.8	79.0	306	4	US-09-147-935A-29	Sequence 29, Appl
40	15.8	79.0	306	4	US-09-147-935A-30	Sequence 30, Appl
41	15.8	79.0	306	4	US-09-147-935A-32	Sequence 32, Appl
42	15.8	79.0	306	4	US-09-147-935A-34	Sequence 34, Appl
43	15.8	79.0	306	4	US-09-147-935A-35	Sequence 35, Appl
44	15.8	79.0	306	4	US-09-147-935A-36	Sequence 36, Appl
45	15.8	79.0	306	4	US-09-147-935A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
; Sequence 70, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750.088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-750-088A-70

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Best Local Similarity 100.0%; Pred. No. 0.23; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0

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Db 1 TACGGTGGCGAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTGGCGAGCTGATCC 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTGGCGAGCTGATCC 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584
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; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||
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RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTGGCGAGCTGATCC 24

RESULT 6
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; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
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;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 50
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

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Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0;

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Db 5 tacggtcgagctgatcc 24
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RESULT 7
US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Anallo
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgagctgatcc 20

Db 18 TACGGTCGGAGCTGATCC 37
|||||

RESULT 8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Anallo
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgagctgatcc 20
|||||

Db 18 TACGGTCGGAGCTGATCC 37
|||||

RESULT 9
US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; Resistance to Rifampin in Mycobacterial Cultures and in

;; TITLE OF INVENTION: Clinical Specimens
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/250,030
;; FILING DATE: 26-MAY-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Muetting, Ann M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 150.105US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggctggcgagctgatcc 20

Db 261 TACGGTCGGCGAGCTGATCC 280

RESULT 10
PCT-US95-06790-1
;; Sequence 1, Application PC/TUS9506790
;; GENERAL INFORMATION:
;; APPLICANT: Mayo Foundation for Medical Education and Research
;; APPLICANT: and Hoffmann-La Roche Inc.
;; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06790
;; FILING DATE: 26-MAY-1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Raasch, Kevin W.
;; REGISTRATION NUMBER: 35,651
;; REFERENCE/DOCKET NUMBER: 150.105WO1

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggctggcgagctgatcc 20

Db 261 TACGGTCGGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
;; Sequence 44, Application US/09147935A
;; Patent No. 6242584
;; GENERAL INFORMATION:
;; APPLICANT: KOOK, Yoon-Hoh
;; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;; FILE REFERENCE: 0136/OF425
;; CURRENT APPLICATION NUMBER: US/09/147,935A
;; PRIOR FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: PCT/KR98/00228
;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 44
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium xenopi
US-09-147-935A-44

Query Match 95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 acggctggcgagctgatcc 20

Db 6 acggctggcgagctgatcc 24

RESULT 12
US-08-750-088A-30
;; Sequence 30, Application US/08750088A
;; Patent No. 6329138
;; GENERAL INFORMATION:
;; APPLICANT: DE BEENHOUWER, HANS
;; APPLICANT: PORTAELS, FRAN OISE
;; APPLICANT: MACHTELINGX, LIEVE
;; APPLICANT: JANNES, GEERT
;; APPLICANT: ROSSAU, RUDI
;; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
;; RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;; NUMBER OF SEQUENCES: 71
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: US

Qy 1 tacggtcggcgagctgatcc 20
||| ||||| ||||| |||||
Db 5 taccqtcqqcgagctgatcc 24

GENERAL INFORMATION:

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:52:14 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20

Sequence: 1 tacggtcggcgagctgatcc 20

Scoring table:

OLIGO_NUC

Gapop 60.0 , Capext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA.*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	US-08-750-088A-70
2	20	100.0	306	4	US-09-147-935A-2
3	20	100.0	306	4	US-09-147-935A-6
4	20	100.0	306	4	US-09-147-935A-7
5	20	100.0	306	4	US-09-147-935A-41
6	20	100.0	306	4	US-09-147-935A-50
7	20	100.0	432	2	US-08-313-185-59
8	20	100.0	432	3	US-09-082-614A-59
9	20	100.0	970	1	US-08-230-030-1
10	20	100.0	970	5	PCT-US95-06790-1
11	19	95.0	306	4	US-09-147-935A-44
12	18	90.0	25	4	US-08-750-088A-30
13	16	80.0	306	4	US-09-147-935A-9
14	16	80.0	306	4	US-09-147-935A-10
15	16	80.0	306	4	US-09-147-935A-13
16	16	80.0	306	4	US-09-147-935A-23
17	16	80.0	306	4	US-09-147-935A-31
18	16	80.0	306	4	US-09-147-935A-39
19	16	80.0	306	4	US-09-147-935A-45
20	16	80.0	306	4	US-09-103-840A-2
21	15	75.0	4403765	4	US-09-103-840A-1
22	15	75.0	4411529	4	US-08-672-158A-10
23	14	70.0	50	1	US-09-147-935A-1
24	14	70.0	306	4	US-08-133-711-43
25	14	70.0	490	1	US-09-426-998-3
26	14	70.0	6822	4	US-09-426-998-4
27	14	70.0			

c

c	28	14	70.0	7741	4	US-09-426-998-4	Sequence 4, Appl
	29	13	65.0	279	1	US-07-612-674-11	Sequence 11, Appl
	30	13	65.0	306	4	US-09-147-935A-12	Sequence 12, Appl
	31	13	65.0	306	4	US-09-147-935A-14	Sequence 14, Appl
	32	13	65.0	306	4	US-09-147-935A-15	Sequence 15, Appl
	33	13	65.0	306	4	US-09-147-935A-16	Sequence 16, Appl
	34	13	65.0	306	4	US-09-147-935A-18	Sequence 18, Appl
	35	13	65.0	306	4	US-09-147-935A-47	Sequence 47, Appl
	36	13	65.0	408	4	US-09-199-637A-222	Sequence 222, Appl
	37	13	65.0	663	1	US-08-506-404D-1	Sequence 1, Appl
	38	13	65.0	663	3	US-09-035-754-1	Sequence 1, Appl
	39	13	65.0	720	3	US-09-094-359-3	Sequence 3, Appl
	40	13	65.0	720	3	US-09-094-359-5	Sequence 5, Appl
	41	13	65.0	720	3	US-09-094-359-7	Sequence 7, Appl
	42	13	65.0	720	3	US-09-094-359-9	Sequence 9, Appl
	43	13	65.0	720	3	US-09-172-063-11	Sequence 11, Appl
	44	13	65.0	720	3	US-09-172-063-12	Sequence 12, Appl
	45	13	65.0	720	3	US-09-172-063-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
; Sequence 70, Application US/08750088A
; Patent No. 6929458
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: JACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657.0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-750-088A-70

Query Match 100.0% Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 1 TACGTCGGCGAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 50
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
|||||

Db 5 tacggtcggcgagctgatcc 24
|||||

RESULT 7

US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20

Db 18 TACGGTCGGCGAGCTGATCC 37
|||||

RESULT 8

US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082.614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356.0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgatcc 20
|||||

Db 18 TACGGTCGGCGAGCTGATCC 37
|||||

RESULT 9

US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; Resistance to Rifampin in Mycobacterial Cultures and in

;; TITLE OF INVENTION: Clinical Specimens
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/250,030
;; FILING DATE: 26-MAY-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Muetting, Ann M.
;; REGISTRATION NUMBER: 33,977
;; REFERENCE/DOCKET NUMBER: 150.105US1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgatcc 20
|||||
Db 261 TACGGTCGCGAGCTGATCC 280

RESULT 10
PCT-US95-06790-1
;; Sequence 1, Application PC/TUS9506790
;; GENERAL INFORMATION:
;; APPLICANT: Mayo Foundation for Medical Education and Research
;; APPLICANT: and Hoffmann-La Roche Inc.
;; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
;; TITLE OF INVENTION: Resistance to Rifampin
;; NUMBER OF SEQUENCES: 15
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Schwegman, Lundberg & Woessner
;; STREET: 3500 IDS Center
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/06790
;; FILING DATE: 26-MAY-1995
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Raasch, Kevin W.
;; REGISTRATION NUMBER: 35,651
;; REFERENCE/DOCKET NUMBER: 150.105W01

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612-339-0331
;; TELEFAX: 612-339-3061
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 970 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgatcc 20
|||||
Db 261 TACGGTCGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
;; Sequence 44, Application US/09147935A
;; Patent No. 6242584
;; GENERAL INFORMATION:
;; APPLICANT: KOOK, Yoon-Hoh
;; APPLICANT: KIM, Bum-Joon
;; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
;; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF IP0B GENE
;; FILE REFERENCE: 0136/OF425
;; CURRENT APPLICATION NUMBER: US/09/147,935A
;; CURRENT FILING DATE: 1999-03-19
;; PRIOR APPLICATION NUMBER: PCT/KR98/00228
;; PRIOR FILING DATE: 1998-07-28
;; NUMBER OF SEQ ID NOS: 50
;; SOFTWARE: KOPATIN 1.0
;; SEQ ID NO 44
;; LENGTH: 306
;; TYPE: DNA
;; ORGANISM: Mycobacterium xenopi
US-09-147-935A-44

Query Match 95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 acggtcgcgcgagctgatcc 20
|||||
Db 6 acggtcgcgcgagctgatcc 24

RESULT 12
US-08-750-088A-30
;; Sequence 30, Application US/08750088A
;; Patent No. 6329138
;; GENERAL INFORMATION:
;; APPLICANT: DE BEENHOUWER, HANS
;; APPLICANT: PORTAELS, FRAN OISE
;; APPLICANT: MACHTELINCKX, LIEVE
;; APPLICANT: JANNES, GEERT
;; APPLICANT: ROSSAU, RUDI
;; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
;; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
;; NUMBER OF SEQUENCES: 71
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
;; STREET: 1100 NEW YORK AVENUE, SUITE 600
;; CITY: WASHINGTON
;; STATE: D.C.
;; COUNTRY: US

TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muetling, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-0361
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcgagctgatcc 20
|||||
Db 261 TACGGTCGGCGAGCTGATCC 280

RESULT 10
PCT-US95-06790-1
Sequence 1, Application PC/TUS9506790
GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105W01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-0361
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcgagctgatcc 20
|||||
Db 261 TACGGTCGGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
Sequence 44, Application US/09147935A
Patent No. 6242584
GENERAL INFORMATION:
APPLICANT: KIM, Bum-Joon
APPLICANT: KIM, Yoon-Hoh
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
PRIOR FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEQ ID NO 44
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium xenopi
US-09-147-935A-44

Query Match 95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 acggtcgcgcgagctgatcc 20
|||||
Db 6 acggtcgcgcgagctgatcc 24

RESULT 12
US-08-750-088A-30
Sequence 30, Application US/08750088A
Patent No. 6329138
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US

; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 50
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggctcggcgagctgatcc 20
|||||

DB 5 tacggctcggcgagctgatcc 24
|||||

RESULT 7

US-08-313-185-59
; Sequence 59, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:

; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: in Mycobacterium Tuberculosis

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/313,185

; FILING DATE: 12-OCT-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggctcggcgagctgatcc 20

DB 18 TACGGTCGGCGAGCTGATCC 37
|||||

RESULT 8

US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:

; APPLICANT: Heym, Beate

; APPLICANT: Cole, Stewart

; APPLICANT: Young, Douglas

; APPLICANT: Zhang, Ying

; APPLICANT: Honore, Nadine

; APPLICANT: Telenti, Amalio

; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

; TITLE OF INVENTION: in Mycobacterium Tuberculosis

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082,614A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/313,185

; FILING DATE: 12-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggctcggcgagctgatcc 20
|||||

DB 18 TACGGTCGGCGAGCTGATCC 37
|||||

RESULT 9

US-08-250-030-1
; Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:

; APPLICANT: Persing, David H.

; TITLE OF INVENTION: Detection of a Genetic Locus Encoding

; TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:48 ; Search time 147.68 Seconds
(without alignments)
33.266 Million cell updates/sec

Title: us-09-786-105-3

Perfect score: 20

Sequence: 1 tacggtcgagcgatgcc 20

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*

4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS.COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	4	US-08-750-088A-70
2	20	100.0	306	4	US-09-147-935A-2
3	20	100.0	306	4	US-09-147-935A-6
4	20	100.0	306	4	US-09-147-935A-7
5	20	100.0	306	4	US-09-147-935A-41
6	20	100.0	306	4	US-09-147-935A-50
7	20	100.0	432	2	US-08-313-185-59
8	20	100.0	432	3	US-09-082-614A-59
9	20	100.0	970	1	US-08-250-030-1
10	20	100.0	970	5	PCT-US95-06790-1
11	19	95.0	306	4	US-09-147-935A-44
12	18	90.0	25	4	US-08-750-088A-30
13	16	80.0	306	4	US-09-147-935A-4
14	16	80.0	306	4	US-09-147-935A-9
15	16	80.0	306	4	US-09-147-935A-10
16	16	80.0	306	4	US-09-147-935A-13
17	16	80.0	306	4	US-09-147-935A-20
18	16	80.0	306	4	US-09-147-935A-23
19	16	80.0	306	4	US-09-147-935A-31
20	16	80.0	306	4	US-09-147-935A-39
21	16	80.0	306	4	US-09-147-935A-45
22	15	75.0	4403765	4	US-09-103-840A-2
23	15	75.0	4411529	4	US-09-103-840A-1
24	14	70.0	50	1	US-08-672-158A-10
25	14	70.0	306	4	US-09-147-935A-1
26	14	70.0	490	1	US-08-133-711-43
27	14	70.0	6822	4	US-09-426-998-3

c

Sequence 4, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 5, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl

US-08-750-088A-70

Patent No. 6920033

GENERAL INFORMATION:

APPLICANT: DE BEENHOUWER, HANS

APPLICANT: PORTAELS, FRAN OISE

APPLICANT: MACHTELINCKX, LIEVE

APPLICANT: JANNES, GEERT

APPLICANT: ROSSAU, RUDI

TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC

TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: US

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/750,088A

FILING DATE: 21-FEB-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: GOLDSTEIN, JORGE A.

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 1657.0010000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

US-08-750-088A-70

ALIGNMENTS

RESULT 1

US-08-750-088A-70

Sequence 70, Application US/08750088A

Patent No. 6920033

GENERAL INFORMATION:

APPLICANT: DE BEENHOUWER, HANS

APPLICANT: PORTAELS, FRAN OISE

APPLICANT: MACHTELINCKX, LIEVE

APPLICANT: JANNES, GEERT

APPLICANT: ROSSAU, RUDI

TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC

TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVENUE, SUITE 600

CITY: WASHINGTON

STATE: D.C.

COUNTRY: US

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/750,088A

FILING DATE: 21-FEB-1997

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: GOLDSTEIN, JORGE A.

REGISTRATION NUMBER: 29,021

REFERENCE/DOCKET NUMBER: 1657.0010000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cdna

US-08-750-088A-70

Query Match 100.0%; Score 20; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 1 TACGGTCGGCGAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

Query Match 100.0%; Score 20; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcggcgagctgattcc 20
|||||
Db 5 tacggtcggcgagctgattcc 24

RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41

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Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 tacggtcggcgagctgattcc 24

RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/OF425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

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; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657-0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-750-088A-30
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 13
US-09-147-935A-4
; Sequence 4, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 4
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US-09-147-935A-4
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Db 9 gtcgagcagctgatcc 24
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RESULT 14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
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; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 9
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9
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Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 15
US-09-147-935A-10
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
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US-09-147-935A-10
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Qy 5 gtcgagcagctgatcc 20
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Db 9 gtcgagcagctgatcc 24
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Search completed: August 7, 2002, 23:51:52
Job time: 7178 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:26 ; Search time 2179.67 Seconds
(without alignments)
192.016 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 tacgctgcgcgcgcgcgcgcgc 20

Scoring table: **CGCG NUC**
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:
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2: gb_htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AF057003	AF057003 Sequence
7	20	100.0	306	6	AF057007	AF057007 Sequence
8	20	100.0	306	6	AF057008	AF057008 Sequence
9	20	100.0	306	6	AF057042	AF057042 Sequence
10	20	100.0	306	6	AF057051	AF057051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	IS0706	IS0706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006564	AE006564 Mycobacte
18	20	100.0	19770	1	MTC1376	295972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AF057045	AF057045 Sequence
21	18	90.0	25	6	A47816	A47816 Sequence 30
22	18	90.0	87	6	AX050338	AX050338 Sequence
23	17	85.0	17407	1	AE006976	AE006976 Mycobacte
24	17	85.0	68848	1	MTV043	AL022004 Mycobacte
25	16	80.0	306	1	AF057456	AF057456 Mycobacte
26	16	80.0	306	1	AF057459	AF057459 Mycobacte
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28	16	80.0	306	1	AF057463	AF057463 Mycobacte
29	16	80.0	306	1	AF057471	AF057471 Mycobacte
30	16	80.0	306	1	AF057473	AF057473 Mycobacte
31	16	80.0	306	1	AF057480	AF057480 Mycobacte
32	16	80.0	306	1	AF057489	AF057489 Mycobacte
33	16	80.0	306	1	AF057496	AF057496 Corynebac
34	16	80.0	306	1	AE173087	AE173087 Mycobacte
35	16	80.0	306	6	AF057005	AF057005 Sequence
36	16	80.0	306	6	AF057010	AF057010 Sequence
37	16	80.0	306	6	AF057011	AF057011 Sequence
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ALIGNMENTS

RESULT 1	AF057450	306 bp	DNA	linear	BCT 17-SEP-1999
LOCUS	Mycobacterium africanum				
DEFINITION	Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.				
ACCESSION	AF057450				
VERSION	AF057450.1	GI:5902487			
KEYWORDS					
SOURCE					
ORGANISM	Mycobacterium africanum.				
REFERENCE					
AUTHORS	Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.				
TITLE	Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)				
JOURNAL	J. Clin. Microbiol.	37 (6),	1714-1720	(1999)	
MEDLINE	99262756				
PUBMED	10325313				
REFERENCE	2 (bases 1 to 306)				
AUTHORS	Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,				

TITLE Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

Location/Qualifiers

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gene
CDS

BASE COUNT

56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgagcgtgacc 20
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Db 5 TACGCTCGGCGAGCTGATCC 24

RESULT 2

AF057451 306 bp DNA linear BCT 17-SEP-1999
LOCUS Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
DEFINITION AF057451
ACCESSION AF057451
VERSION AF057451.1 GI:5902489
KEYWORDS
SOURCE Mycobacterium bovis.
ORGANISM Mycobacterium bovis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

REFERENCE

AUTHORS

TITLE

2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

JOURNAL

MEDLINE

PUBMED

99262756

10325313

2 (bases 1 to 306)

Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

source

Location/Qualifiers
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gene

CDS

56 a 95 c 108 g 47 t

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BASE COUNT

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Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgagcgtgacc 20
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Db 5 TACGCTCGGCGAGCTGATCC 24

RESULT 3

AF057452 306 bp DNA linear BCT 17-SEP-1999
LOCUS Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
DEFINITION AF057452
ACCESSION AF057452
VERSION AF057452.1 GI:5902491
KEYWORDS
SOURCE Mycobacterium bovis BCG.
ORGANISM Mycobacterium bovis BCG.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

REFERENCE

AUTHORS

TITLE

2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

JOURNAL

MEDLINE

PUBMED

99262756

10325313

2 (bases 1 to 306)

Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youn-gon-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

source

Location/Qualifiers
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/strain="French 1173P2"
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gene

CDS

56 a 95 c 108 g 47 t

BASE COUNT

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgctcgagcgtgacc 20
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DB 5 TACGGTCGGCGAGCTGATCC 24

RESULT 4

LOCUS AF057453 306 bp DNA linear BCT 17-SEP-1999

DEFINITION Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057453

VERSION AF057453.1 GI:5902493

KEYWORDS

SOURCE Mycobacterium bovis BCG.

ORGANISM Mycobacterium bovis BCG.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

TITLE J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL 99262756

MEDLINE 10325313

REFERENCE 2 (bases 1 to 306)
Kook,Y.H., Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H.,
Kim,S.-J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

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Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 5

LOCUS AF057454 306 bp DNA linear BCT 08-OCT-1999

DEFINITION Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.

ACCESSION AF057454

VERSION AF057454.1 GI:5902495

KEYWORDS

SOURCE Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

TITLE J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL 99262756

MEDLINE 10325313

REFERENCE 2 (bases 1 to 306)
Kook,Y.H., Kim,B.-J., Lee,S.H., Lyu,M.A., Kim,S.-J., Bai,G.H.,
Kim,S.-J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

TITLE Direct Submission

JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES

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BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 6

LOCUS AR157003 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 2 from patent US 6242584.

ACCESSION AR157003

VERSION AR157003.1 GI:15125707

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 306)
Kook,Y. and Kim,B.
Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene
Patent: US 6242584-A 2 05-JUN-2001;
Location/Qualifiers

FEATURES

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BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 7
LOCUS ARI57007 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION ARI57007
VERSION ARI57007.1 GI:15125711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y.-H. and Kim,B.-J.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
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Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 8
LOCUS ARI57008 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6242584.
ACCESSION ARI57008
VERSION ARI57008.1 GI:15125712
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 9
LOCUS ARI57042 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION ARI57042
VERSION ARI57042.1 GI:15125746
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 10
LOCUS ARI57051 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION ARI57051
VERSION ARI57051.1 GI:15125755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
source 1..306
/organism="unknown"
BASE COUNT 56 a 94 c 108 g 48 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcggcgagctgattcc 20
|||||
Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 11
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37)
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 34:1, 647-650 (1993)

FEATURES

Location/Qualifiers

1..432 /organism="Mycobacterium tuberculosis"

/strain="H37"

/db_xref="taxon:1773"

CDS

<1..>432

/codon_start=1

/transl_table=1

/product="RNA polymerase beta subunit"

/protein_1d="AAB58068.1"

/db_xref="GI:149992"

/translation="GNRLRTVGLIQNIVGHSRMERYRRTTODVEAITPQTL
INIRPVVAIKEFGTQSOFMDONNLSGLTHKRLSALGPGGLSRRAGLEVRDV
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149

/phenotype="rifampicin resistant in association with
mutation 234 G"

/replace="C"

188

/phenotype="rifampicin resistant"

/replace="C"

191

/phenotype="rifampicin resistant in association with
mutation 203 T"

/replace="C"

194

/phenotype="rifampicin resistant"

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203

/phenotype="rifampicin resistant"

/replace="C"

208..210

/phenotype="rifampicin resistant"

/replace="a"

232

/phenotype="rifampicin resistant"

/replace="g"

232

/phenotype="rifampicin resistant"

/replace="a"

233

/phenotype="rifampicin resistant"

/replace="g"

233

/phenotype="rifampicin resistant"

/replace="C"

234

/phenotype="rifampicin resistant"

/replace="g"

247..248

/phenotype="rifampicin resistant"

/replace="ca"

248

/phenotype="rifampicin resistant"

/replace="g"

248

/phenotype="rifampicin resistant"

/replace="t"

254

/phenotype="rifampicin resistant"

/replace="C"

140 C

148 g

67 t

BASE COUNT

ORIGIN

Query Match

100.0%; Score 20; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcgtgatcc 20

DB 18 TACGTCGCGAGCTGATCC 37

RESULT 12

LOCUS

AR067448

SEQUENCE

59 from patent US 5851763.

ACCESSION

AR067448

VERSION

AR067448.1

KEYWORDS

GI:5998670

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 432)

AUTHORS

Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and
Bodmer,T.

TITLE

Rapid detection of antibiotic resistance in mycobacterium
tuberculosis

JOURNAL

Patent: US 5851763-A 59 22-DEC-1998;

FEATURES

Location/Qualifiers

1..432

BASE COUNT

77 a 139 c 149 g 67 t

ORIGIN

Query Match

100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcgtgatcc 20

DB 18 TACGTCGCGAGCTGATCC 37

RESULT 13

LOCUS

I50706

SEQUENCE

1 from patent US 5643723.

ACCESSION

I50706

VERSION

I50706.1

KEYWORDS

GI:2472409

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 970)

AUTHORS

Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
and Whelan,A.Christian.

TITLE

Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens

JOURNAL

Patent: US 5643723-A 1 01-JUL-1997;

FEATURES

Location/Qualifiers

1..970

BASE COUNT

182 a 302 c 330 g 156 t

ORIGIN

Query Match

100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 3.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcgtgatcc 20

DB 261 TACGTCGCGAGCTGATCC 280

RESULT 14

LOCUS

AX111339

SEQUENCE

3534 bp DNA

DEFINITION

Sequence 2072 from Patent WO0123604.

ACCESSION

AX111339

VERSION

AX111339.1

KEYWORDS

GI:13927631

SOURCE

Mycobacterium tuberculosis.

Linear PAT 30-APR-2001

ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 3534)
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2072 05-APR-2001;
FEATURES Infectio Diagnostic (I.D.I.) INC. (CA)
source Location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggtcgcgcgagctgaccc 20
|||||
Db 1137 TACGCTCGCGAGCTGATCC 1156
RESULT 15
MTU12205 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 3853)
AUTHORS Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
Cole,S., Schopfer,K. and Burkart,T.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3853)
AUTHORS Imboden,P.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
FEATURES Location/Qualifiers
1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
576..>3853
/gene="rpoB"
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/protein_id="AA02042.2"
/db_xref="GI:714499"
/translation="MLEGCIADSRGSKTAASPSRPOSSNNNSVGPANRYSPAKL
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TEKGTIINGTERVAVSOLVSPGVTDFETIDKSTDKTLHSVKVTPSRGAMLEFDYDK
KDIVGVIRDRKRPQTVLLKALGVTSEQIVERTSEIMRSTLEKNDTVGTDEALLD
IYRKLREGEPTKESQTLLENLEFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSLT

EDVAVATETIYVRLHEGOTTTPVPGVVEVETDDIDHFGNRLRTVIGELIQNDIRVG
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FGLETETPVKAVDGVSDGIYLTADDEDHRYVAQANSPIDADRFVPEVPLVRRAG
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LVGTGMELRAALDAATSSSOESGVIEEVASDYITVMHNDCTRRTYRKRARSNHGIC
ANOCPIYDADQDRVACGVITADGECTDGEALGKNLVAIMPEGHNTEDATILSNRL
VEEDVLSIHIEHEIDARDTKLSAEITTDIPNISDEVLADDERGIVIRIGAEVRDG
DILVGYTPKGETELTPEERLLRAIFEGKAREVDTSLKVPHSGSKVIGIRVFSRED
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TPVPDGAOEALDGLSCTLPNRGDVLYVADGKAMLFDCRSRGPPEPYPTVVMYTM
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TIKS"
BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggtcgcgcgagctgaccc 20
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Db 1712 TACGCTCGCGAGCTGATCC 1731

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Job time: 9215 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 20:08:01 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 taacgctgcgcagcgtatcc 20

Scoring table:

OLIGO_NUC
Gapop 60.0 , Gapect 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estcu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estt2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	422	10	BE443802 WHE1122_B
2	17	85.0	544	10	BE445100 WHE1132_H
3	17	85.0	538	10	BE444713 WHE1137_H
4	17	85.0	610	9	BE195103 BE195103 HVSMEH008
5	17	85.0	658	10	BE442518 WHE1101_H
6	17	80.0	828	10	BG299722 HVSME002
7	16	80.0	130	10	BM397871 BM397871
8	16	80.0	132	10	BM396091 BM396091
9	16	80.0	134	10	BM396255 BM396255
10	16	80.0	606	10	BE1981973 BE1981973
11	16	80.0	640	10	BE188442 BE188442
12	16	80.0	708	10	BE585978 BE585978
13	15	75.0	237	10	BE423869 BE423869
14	15	75.0	376	9	AT945868 AT945868
15	15	75.0	379	9	AT944952 AT944952
16	15	75.0	556	12	BH229591 BH229591
17	15	75.0	568	10	BE628597 BE628597

18	15	75.0	652	10	BE489438 BE489438
19	15	75.0	655	10	BE489430 BE489430
20	15	75.0	667	10	BE489536 BE489536
21	15	75.0	703	10	BE496035 BE496035
22	15	75.0	722	10	BE496005 BE496005
23	15	75.0	958	10	BE969326 BE969326
24	15	75.0	984	12	CNS01G72 CNS01G72
25	15	75.0	1000	10	BG416363 BG416363
26	15	75.0	1188	10	BM477266 BM477266
27	14	70.0	159	10	BE1727507 BE1727507
28	14	70.0	180	10	C61884 C61884
29	14	70.0	239	10	BE920601 BE920601
30	14	70.0	251	12	A0906217 A0906217
31	14	70.0	252	10	W87730 W87730
32	14	70.0	292	9	BB347857 BB347857
33	14	70.0	299	10	BE113481 BE113481
34	14	70.0	318	10	M79472 M79472
35	14	70.0	328	9	AW922029 AW922029
36	14	70.0	329	10	H57342 H57342
37	14	70.0	339	9	AJ781216 AJ781216
38	14	70.0	344	10	BE415176 BE415176
39	14	70.0	349	9	AU110574 AU110574
40	14	70.0	349	10	BG274757 BG274757
41	14	70.0	352	10	T83696 T83696
42	14	70.0	360	9	AV186178 AV186178
43	14	70.0	360	9	AV191317 AV191317
44	14	70.0	360	9	AV192208 AV192208
45	14	70.0	360	9	AV197881 AV197881

ALIGNMENTS

RESULT 1	BE443802	422 bp	mRNA	linear	EST 25-JUL-2000
LOCUS	WHE1122_B06_C12Z5	Wheat etiolated seedling root	normalized	CDNA	
DEFINITION	Library Triticum aestivum	CDNA clone	WHE1122_B06_C12	mRNA	
ACCESSION	BE443802				
VERSION	BE443802.1	GI:9443341			
KEYWORDS	EST.				
SOURCE	bread wheat.				
ORGANISM	Triticum aestivum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae				
AUTHORS	Anderson,O.D., Chao,S., Chol,D.W., Close,T.J., Fenton,R.D., Han				
TITLE	1 (bases 1 to 422)				
JOURNAL	Rausch,C.D., Seaton,C.L., Tong,J.C. and Zhang,D.				
COMMENT	The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library				
UNPUBLISHED (2000)	Contact: Olin Anderson				
US Department of Agriculture, Agriculture Research Service, Pacific					
West Area, Western Regional Research Center					
800 Buchanan Street, Albany, CA 94710, USA					
Tel: 5105595773					
Fax: 5105595818					
Email: oanderson@w.usda.gov					
Sequence have been trimmed to remove vector sequence and low					
quality sequence with phred score less than 20					
Seq primer: Scratagene SK primer.					
Location/Qualifiers					
1..422					
/organism="Triticum aestivum"					
/cultivar="Chinese Spring"					
/db_xref="taxon:455"					
/clone="WHE1122_B06_C12"					
/clone_lib="Wheat etiolated seedling root normalized CDNA					
library"					
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/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pbuascript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared. A cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pbuascript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
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BASE COUNT 84 a 130 c 124 g 84 t

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggtcgcgcagctgattcc 20
|||||

Db 86 ggtcgcgcagctgattcc 102

RESULT 2
BE445100 544 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1132_H08_P16Z5 Wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
sequence.
ACCESSION BE445100
VERSION BE445100
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 544)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"

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/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pbuascript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared. A cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pbuascript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
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BASE COUNT 121 a 173 c 132 g 118 t

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggtcgcgcagctgattcc 20
|||||

Db 512 ggtcgcgcagctgattcc 528

RESULT 3
BE444713 558 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1137_H03_005Z5 Wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713
VERSION BE444713
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 558)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..558
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
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/lab_host="E. coli DH10B"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pbuascript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were

surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the *TJ* Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give plasmid preparations before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ggtcggcagcgtcatcc 20
|||||
Db 514 GGTGGCGAGCTGATCC 530

RESULT 4
LOCUS BE195103 610 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEH0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCMDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEH0088E21f,
mRNA sequence.

ACCESSION BE195103 GI:16321083
VERSION BE195103.3
KEYWORDS
SOURCE
ORGANISM

Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
1 (bases 1 to 610)
Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total bp bases = 238
Seq primer: AATTAACTCCTCCTAAAGCG
High quality sequence stop: 563.
Location/Qualifiers

FEATURES
source
1..610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEH0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCMDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP. Site_1: EcoRI; Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,

BASE COUNT 127 a 203 c 158 g 120 t
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ggtcggcagcgtcatcc 20
|||||
Db 499 GGTGGCGAGCTGATCC 515

RESULT 5
LOCUS BE442518 658 bp mRNA linear EST 25-JUL-2000
DEFINITION WHE1101_H10_O192S Wheat etiolated seedling root normalized cDNA
library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA
sequence.

ACCESSION BE442518 GI:9442034
VERSION BE442518.1
KEYWORDS
SOURCE
ORGANISM

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 658)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragagene SK primer.
Location/Qualifiers

FEATURES
source
1..658
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_O19"
/clone_lib="Wheat etiolated seedling root normalized cDNA
library"

```

/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/Note="Vector: Lambda Uni-ZAP XR, excised phagemid
pluscript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TU Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pluscript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```

```

BASE COUNT      144 a      209 c      105 g      140 t
ORIGIN

Query Match      85.0%; Score 17; DB 10; Length 658;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4      ggtcgagcagctgctcc 20
          ||||||||||||||||
Db      512      GGTGCGCGAGCTGATCC 528
```

```

RESULT 6      BG299722      828 bp      mRNA      linear      EST 17-OCT-2001
LOCUS      HVSMEa0021120f Hordeum vulgare seedling shoot EST library
DEFINITION  HVCNDA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
              mRNA sequence.
ACCESSION  BG299722
VERSION    BG299722.1 GI:13087434
KEYWORDS   EST.
SOURCE     barley.
ORGANISM   Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Hordeum.
            1 (bases 1 to 828)
REFERENCE  Wing, R., Close, T.J., Kleinholz, A., Wise, R., Begum, D., Frisch, D., Yu
            , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
            Fenton, R.D. and Main, D.
            Development of a genetically and physically anchored EST resource
            for barley genomics: Morex cold-stressed seedling shoot cDNA
            library
            Unpublished (2001)
JOURNAL    Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: twing@clemson.edu
            Total bp bases = 574
            Seq primer: AATTAAACCTCAGTAAGG
            High quality sequence stop: 643.
            Location/Qualifiers
            1..828
            /organism="Hordeum vulgare"
            /cultivar="Morex"
            /db_xref="taxon:4513"
            /clone="HVSMEa0021120f"
            /clone_lib="Hordeum vulgare seedling shoot EST library
            HVCNDA0001 (Cold stress)"
            /tissue_type="Seedling shoot"
```

```

/lab_host="TJc121"
/Note="Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
Seeds were surface sterilized then germinated under axenic
conditions in the dark at room temperature on filter paper
with water, nystatin and cefotaxime in covered
crystallization dishes. Five-day old seedlings were
incubated at 50c for 2 days. Shoots were then harvested,
total RNA was prepared, poly(A) RNA was purified, one
primary unamplified cDNA library was made, and 600000 pfu
were in vivo excised to give pluscript SK(-) cDNA
phagemids. These steps were performed in the TU Close
laboratory at the University of California, Riverside
(Choi, Close, Fenton). Phagemids were plated and picked at
the Clemson University Genomics Institute (CUGI) (Begum,
Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
, DNA sequencing and sequence analysis were performed at
CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinholz A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)"
```

```

BASE COUNT      172 a      271 c      220 g      165 t
ORIGIN

Query Match      85.0%; Score 17; DB 10; Length 828;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4      ggtcgagcagctgctcc 20
          ||||||||||||||||
Db      500      GGTGCGCGAGCTGATCC 516
```

```

RESULT 7      BM397871      130 bp      mRNA      linear      EST 17-JAN-2002
LOCUS      BM397871/c
DEFINITION  5009-0-36-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397871
VERSION    BM397871.1 GI:18197924
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila.
            Tetrahymena thermophila.
            ORGANISM   Tetrahymena thermophila.
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomata; Tetrahymenina; Tetrahymena.
            1 (bases 1 to 130)
REFERENCE  Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Klirk, K.E., Frankel
            , J. and Klobutcher, L.
            EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
JOURNAL    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
            Location/Qualifiers
            1..130
            /organism="Tetrahymena thermophila"
            /strain="CU428.1"
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /Note="Vector: Bluescript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
```


Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 26 a 41 c 44 g 18 t 1 others

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 130;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gtcggcgcagctgattcc 20
 |||||||
 Db 90 GTCGGCGAGCTGATCC 75

RESULT 8
 BM396091/c 132 bp mRNA linear EST 17-JAN-2002
 LOCUS
 DEFINITION 5009-0-17-B01.t.1 Chllocoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM396091
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Tetrahymena thermophila.
 Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 132)
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apurkew@midway.uchicago.edu
 Seq primer: 73.

FEATURES
 Source
 1. 132
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chllocoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chllocoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 27 a 42 c 44 g 19 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 132;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gtcggcgcagctgattcc 20
 |||||||
 Db 92 GTCGGCGAGCTGATCC 77

RESULT 9
 BM398255/c 134 bp mRNA linear EST 17-JAN-2002
 LOCUS
 DEFINITION 5009-0-42-H08.t.1 Chllocoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398255
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Tetrahymena thermophila.
 Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 1 (bases 1 to 134)
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel, J., and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apurkew@midway.uchicago.edu
 Seq primer: 73.

FEATURES
 Source
 1. 134
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_lib="Chllocoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chllocoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 26 a 44 c 46 g 18 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 134;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gtcggcgcagctgattcc 20
 |||||||
 Db 94 GTCGGCGAGCTGATCC 79

RESULT 10
 BI981973/c 606 bp mRNA linear EST 24-OCT-2001
 LOCUS
 DEFINITION 513f08.y1 zebrafish adult brain Dario rerio cDNA clone 533151 5'
 similar to TR:Q9Y4D4 Q9Y4D4 KIA0648 PROTEIN ; mRNA sequence.
 BI981973
 BI981973.1 GI:16371108
 EST.
 zebrafish.
 Dario rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Dario.

REFERENCE
 AUTHORS
 Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.

TITLE
 JOURNAL
 COMMENT
 WashU zebrafish EST Project 1998
 Unpublished (1998)
 Other_ESTs: fu53f08.x1
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu
 cDNA Library Preparation: John Neal, cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone distribution: Genome Systems, St. Louis.
 Misouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Resourcezentrum Primatendatenbank, Berlin, Germany (web address:
 www.rzpd.de)
 High quality sequence stop: 446.

FEATURES
source
Location/Qualifiers
1..606
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5333151"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/note="Vector: pZiPlox; Site_1: NotI; Site_2: SalI.
Original library was constructed in lambdaZiPlox. Mass
excision of the cDNA library was performed to yield
pZiPlox plasmids. Insert check was done in original
library."

BASE COUNT 209 a 133 c 139 g 125 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 606;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctg 16
|||||

Db 452 TACGCTCGCGAGCTG 437

RESULT 11 640 bp mRNA linear EST 12-OCT-2001
BI888442
LOCUS ZF637-2-000197 zebrafish shield stage whole embryo cDNA library
DEFINITION MPMP637 Danio rerio cDNA clone MPMP637_18E17;MPMP637E1718 5',
mRNA sequence.
ACCESSION BI888442
VERSION BI888442.1 GI:16095713
KEYWORDS EST.
SOURCE zebrafish.
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 640)
Clark, M., Anstad, P., Hennig, S., Johnson, S.L. and Lehrach, H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)
JOURNAL Contact: Hennig S
laboratory 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Inhestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 640.
Location/Qualifiers
1..640
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="MPMP637_18E17;MPMP637E1718"
/clone_lib="zebrafish shield stage whole embryo cDNA
library MPMP637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E. coli, XL1 blue MRF"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed. SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"

BASE COUNT 209 a 152 c 139 g 139 t 1 others

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 640;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctg 16
|||||

Db 541 TACGCTCGCGAGCTG 526

RESULT 12 708 bp mRNA linear EST 17-AUG-2000
BE585978
LOCUS BE585978
DEFINITION Est#7PT7_A09.a9_065 KSU wheat Fusarium graminearum infected spike
cDNA library Trilicium aestivum cDNA clone Est#7PT7_A09.a9_065, mRNA
sequence.
ACCESSION BE585978
VERSION BE585978.1 GI:9839010
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triliceae; Trilicium.
1 (bases 1 to 708)
Fellers, J.P., Li, W.L., Hill-Ambroz, K., Matthews, A. and Gill, B.S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
Unpublished (2000)
JOURNAL Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@fallita.ksu.edu
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: T7.
Location/Qualifiers
1..708
/organism="Trilicium aestivum"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/clone="Est#7PT7_A09.a9_065"
/clone_lib="KSU wheat Fusarium graminearum infected spike
cDNA library"
/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli JM109"
/note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;
Plants were grown in the greenhouse. Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartRt PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT 154 a 221 c 177 g 156 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 708;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 gtgcgcgcagctgctcc 20
|||||

Db 559 GTGCGCGAGCTGATCC 574

RESULT 13
BE423869/c
LOCUS
DEFINITION
WHE0067_F05_K0925 wheat endosperm cDNA library Triticum aestivum
BE423869
ACCESSION
BE423869
VERSION
BE423869.1 GI:9421712
KEYWORDS
EST.
SOURCE
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
Triticaceae; Triticum.
1 (bases 1 to 237)
Altenbach, S., Anderson, O.D., Chao, S., Gall, G., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
REFERENCE
Auteurs
The structure and function of the expressed portion of the wheat genomes - Endosperm cDNA library
Unpublished (2000)
COMMENT
JOURNAL
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: candersn@w.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
1..237
/organism="Triticum aestivum"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0067_F05_K09"
/clone_1lb="Wheat endosperm cDNA library"
/tissue="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli SOLR"
/note="Vector: Lambda ZAP II, excised phagemid; Site_1: EcoRI; Seeds collected, endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."

BASE COUNT
ORIGIN
65 a 79 c 40 g 53 t

Query Match
Best Local Similarity 100.0%; Score 15; DB 10; Length 237;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 tcgagcagctgaccc 20
|||||
Db 79 TCGCGAGCTGATCC 65

RESULT 14
AI945868
LOCUS
DEFINITION
bs17607.y1 Drosophila melanogaster adult testis library Drosophila
melanogaster cDNA clone bs17607 5', mRNA sequence.
AI945868
ACCESSION
AI945868.2 GI:9991196
VERSION
AI945868.2
KEYWORDS
EST.
SOURCE
ORGANISM
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 376)
Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and

TITLE
JOURNAL
MEDLINE
COMMENT
Oliver, B.
Gene discovery using computational and microarray analysis of transcription in the drosophila melanogaster testis
Genome Res. 10 (12), 2030-2043 (2000)
20568492
On Aug 17, 1999 this sequence version replaced gi:5736266.
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@helix.nih.gov,
http://www.nidk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National Institute of Diabetes and Digestive and Kidney Diseases, NIH (see http://www.nidk.nih.gov/intram/people/boliver.htm). DNA sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 17 row: 9 column: 07
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..376
/organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/y"
/db_xref="taxon:7227"
/clone="bs17607"
/clone_1lb="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/note="Organ: testis. Vector: pBluescript SK (Stratagene); Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5 day adult y[*] w[67c1]/y males raised at 25°C. RNA isolated using Trizol (Life Technologies) and a single round of Poly(A)+ selection using Oligotex (Qiagen). cDNA library constructed using Stratagene ZAP-cDNA synthesis kit. Oligo dt-primed, size fractionated -1-6 kb, and directionally cloned at EcoRI and XhoI in Uni-ZAP XR. Following a single round of amplification pBluescript SK phagemids were mass excised. A distribution channel for clones is being sought, but not currently available. Requests for clones cannot be honored."

BASE COUNT
ORIGIN
110 a 94 c 107 g 65 t

Query Match
Best Local Similarity 100.0%; Score 15; DB 9; Length 376;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 acggtcggcagctg 16
|||||
Db 272 ACGTGGCGAGCTG 286

RESULT 15
AI944952
LOCUS
DEFINITION
bs07c12.y1 Drosophila melanogaster adult testis library Drosophila
melanogaster cDNA clone bs07c12 5', mRNA sequence.
AI944952
ACCESSION
AI944952.2 GI:9990300
VERSION
AI944952.2
KEYWORDS
EST.
SOURCE
ORGANISM
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 379)
Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and
Oliver, B.
Gene discovery using computational and microarray analysis of transcription in the drosophila melanogaster testis

JOURNAL
MEDLINE
20568492
Genome Res. 10 (12), 2030-2043 (2000)
On Aug 17, 1999 this sequence version replaced gi:5735350.
COMMENT

Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliverbhelix.nih.gov,
<http://www.nidddk.nih.gov/intram/people/poliver.htm>
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
<http://www.nidddk.nih.gov/intram/people/poliver.htm>). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
Plate: 07 row: c column: 12
Seq primer: M13RPL reverse primer (ABI).

FEATURES

Source

1. .379
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/organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/y"
/db_xref="taxon:7227"
/clone="bs07c12"
/clone_lib="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/note="Organ: testis; Vector: pBluescript SK (Stratagene);
Site.1: EcoR I; Site.2: Xho I; Testes dissected from 1-5
day adult y[*] w[67c1]/y males raised at 25°C. RNA
isolated using RNeasy (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Stratagene ZAP-cDNA synthesis
kit. Oligo dt-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

BASE COUNT 104 a 96 c 113 g 66 t
ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 379;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 acggtcggcgagctg 16
|||||
Db 39 ACGGTGGCGGAGCTG 53

Search completed: August 7, 2002, 23:12:30
Job time: 11069 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:30 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20
Sequence: 1 taagcgcttcgatgacc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 674847542 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST:*
1: em_estdb:*
2: em_esthum:*
3: em_estnu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	234	10	W06754 SMEST0390 S
2	17	85.0	579	10	T24127 SMEST0325 S
3	16	80.0	624	10	BE896357 B01439015
4	15	75.0	384	10	BM077908 PB21906.Y
5	15	75.0	452	9	AM694629 NF078E03S
6	15	75.0	517	12	TA247H04P
7	15	75.0	536	12	A0783856 HS_2001_A
8	15	75.0	537	12	TA140G03P
9	15	75.0	540	12	TA190A10P
10	15	75.0	631	12	BH615799 T. brucei
11	15	75.0	690	9	BE053145 GA_Ea000
12	15	75.0	1033	12	CNSD404YP
13	15	75.0	1218	10	BM0071170
14	14	70.0	247	9	AV640031
15	14	70.0	269	9	AV640876
16	14	70.0	288	9	BB177553
17	14	70.0	336	12	AQ660540 Sheared D

C	18	14	70.0	390	9	AV644609	AV644609
C	19	14	70.0	416	9	AJ284239	AJ284239
C	20	14	70.0	421	12	A2813806	A2813806
C	21	14	70.0	428	10	BK252718	BK252718
C	22	14	70.0	431	9	AW280184	AW280184
C	23	14	70.0	466	9	AF051116	AF051116
C	24	14	70.0	472	10	BE449520	BE449520
C	25	14	70.0	474	9	AV396989	AV396989
C	26	14	70.0	476	9	A1483656	A1483656
C	27	14	70.0	477	9	A1488127	A1488127
C	28	14	70.0	489	9	AM618736	AM618736
C	29	14	70.0	497	9	AV643117	AV643117
C	30	14	70.0	508	9	AV642711	AV642711
C	31	14	70.0	518	9	AV642141	AV642141
C	32	14	70.0	525	9	AM650840	AM650840
C	33	14	70.0	531	9	AV642766	AV642766
C	34	14	70.0	544	12	AQ843909	AQ843909
C	35	14	70.0	556	9	AM155814	AM155814
C	36	14	70.0	562	12	BH487728	BH487728
C	37	14	70.0	566	9	AV631818	AV631818
C	38	14	70.0	582	12	CNS01K68	AV631818
C	39	14	70.0	626	9	AM442770	AM442770
C	40	14	70.0	626	9	BB640393	BB640393
C	41	14	70.0	628	10	BE270176	BE270176
C	42	14	70.0	664	10	BG102752	BG102752
C	43	14	70.0	670	12	AQ943645	AQ943645
C	44	14	70.0	672	12	AQ943372	AQ943372
C	45	14	70.0	676	9	A1491107	A1491107

ALIGNMENTS

RESULT 1
W06754/c 234 bp mRNA linear EST 01-JUL-1996
LOCUS SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION W06754
VERSION W06754.1 GI:1444974
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS Franco,G.R. and Pena,S.D.J.
TITLE Unpublished
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimica e Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
Location/Qualifiers

FEATURES
source
1..234
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="Caxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and

Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (lambda BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaa 17
|||||

DB 64 TACGGCGTTTCGATGAA 48

RESULT 2 579 bp mRNA linear EST 27-FEB-1995
T24127
LOCUS SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
T24127
VERSION T24127.1 GI:529730
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni.
REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma. 1 (bases 1 to 579)
AUTHORS Franco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C. and Pena, S.D.J.
TITLE Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library
JOURNAL Gene 152, 141-147 (1995)
MEDLINE 95137379
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Biologia
Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
Location/Qualifiers
1. 579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houbeline, L. M. Biofeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid DNA (lambda BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaa 17
|||||

DB 75 TACGGCGTTTCGATGAA 59

RESULT 3 624 bp mRNA linear EST 20-OCT-2000
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LOCUS 601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5',
DEFINITION mRNA sequence.
ACCESSION BE896357
VERSION BE896357.1 GI:10360678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 624)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DC/DMP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers
1. 624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH-MGC-72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPOr6; Site_1: NotI; Site_2: SalI; cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies." "Technologies." "

BASE COUNT 155 a 209 c 150 g 110 t

ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 gcggttcgatgacc 20
|||||

DB 582 GCGTTTCGATGACCC 597

```

RESULT 4
LOCUS BM077908 384 bp mRNA linear EST 14-NOV-2001
DEFINITION p51g06.y1 Ancylostoma caninum L3 SS SL1 TOPO V1 Murphy Chiapelli
            McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
ACCESSION BM077908
VERSION   BM077908.1 GI:16924944
KEYWORDS EST.
SOURCE    dog hookworm.
ORGANISM  Ancylostoma caninum
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Strongyliida;
            Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 384)
AUTHORS   McCarter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J., Wylie,T.,
            Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,T.,
            Gibbons,M., Rittler,E., Bennett,J., Franklin,C., Tsagarisshvili,R.,
            Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,R., Steptoe
            ,M., Allen,M., Person,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S.,
            Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and
            Wilson,R.
            The Washington Univ. Nematode EST Project, 1999
            Unpublished (1999)
            Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@wustl.wustl.edu
            The library was constructed by Claire Murphy, Brandi Chiapelli, and
            Dr. James McCarter at Washington University, St. Louis. DNA
            Sequencing by: Washington University Genome Sequencing Center.
FEATURES
    source
        1..384
            /organism="Ancylostoma caninum"
            /db_xref="taxon:29170"
            /clone_lib="Ancylostoma caninum L3 SS SL1 TOPO V1 Murphy
            Chiapelli McCarter"
            /dev_stage="Serum stimulated L3"
            /lab_host="DH10B"
            /note="Vector: PCR11-TOPO (Invitrogen); Site:1: EcoRI;
            Site:2: EcoRI; The library was constructed by Claire
            Murphy, Brandi Chiapelli, and Dr. James McCarter at
            Washington University, St. Louis. Oligo(dT)-SL1 PCR based
            library. Ancylostoma caninum SS/LS cDNA PCR products of
            size >400 nucleotides containing SL1 on the 5' end and
            oligo(dT) on the 3' end were non-directionally cloned
            into PCR11-TOPO(Invitrogen) following the TOPO TA cloning
            protocol. Nematodes were provided by Dr. Prema Arasu
            (Prema.Arasu@ncsu.edu) of North Carolina State University
            in Raleigh, NC."
BASE COUNT 116 a 71 c 85 g 112 t
ORIGIN
Query Match 75.0%; Score 15; DB 10; Length 384;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 ggcgttcgacgaac 18
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    Db 324 GCGCTTCGATGAC 338
RESULT 5
LOCUS AM694629 452 bp mRNA linear EST 21-DEC-2000
DEFINITION NF078E03ST1021 Developing stem Medicago truncatula cDNA clone
ACCESSION AM694629
VERSION   AM694629.2 GI:11957636

```

```

KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
            Medicago.
REFERENCE 1 (bases 1 to 452)
AUTHORS   He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
            ,C.J., Flores,H.R., Imman,J.T., Weller,J.W., May,G.D. and Dixon
            ,R.A.
            Expressed Sequence Tags from the Samuel Roberts Noble Foundation
            Medicago truncatula stem library
            Unpublished (2000)
            On Apr 14, 2000 this sequence version replaced gi:7569391.
TITLE
JOURNAL
COMMENT
    Contact: Dixon RA
    Plant Biology Division
    The Samuel Roberts Noble Foundation
    2510 Sam Noble Parkway, Ardmore, OK 73402, USA
    Tel: 580 221 7302
    Fax: 580 221 7380
    Email: radixon@noble.org
    Insert Length: 736 Std Error: 0.00
    Plate: 078 row: E column: 03
    Seq primer: TCACACAGGAACACGCTATGAC.
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            /db_xref="taxon:3880"
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            /clone_lib="Developing stem"
            /tissue_type="stem"
            /dev_stage="Pooled developmental"
            /note="Vector: Lambda zap; Contains a mixture of
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BASE COUNT 152 a 94 c 91 g 115 t
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Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 gcttcgatgaacc 20
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    Db 338 CTTTCGATGACCC 324
RESULT 6
LOCUS TA247H04P 517 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 247H04, forward sequence,
            genomic survey sequence.
ACCESSION AL483262
VERSION   AL483262.1 GI:11848938
KEYWORDS GSS.
SOURCE    Trypanosoma brucei.
ORGANISM  Trypanosoma brucei
            Eukaryota; Eulenzozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE 1 (bases 1 to 517)
AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
            Direct Submission
            Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh@sanger.ac.uk
            Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREG927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (

```

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@ligr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
SOURCE
1. 517
Location/Qualifiers

BASE COUNT
116 a 116 c 135 g 150 t
ORIGIN
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="247h04"

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Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaac 18
|||||
Db 293 GGCCTTCGATGAAC 307

RESULT 7
AO783856 536 bp DNA linear GSS 03-AUG-1999
LOCUS
DEFINITION HS.2001_A2_F09_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=18 Row=K, DNA sequence.
ACCESSION AO783856
VERSION AO783856.1 GI:5691480
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 536)
Mahaitsas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Hood L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)

JOURNAL
MEDLINE
COMMENT Contact: Mahaitsas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2001 row: K column: 18
Seq Primer: T7
Class: BAC ends
High quality sequence stop: 536.
Location/Qualifiers

FEATURES
SOURCE
1. 536
Location/Qualifiers

BASE COUNT
160 a 124 c 92 g 156 t 4 others
ORIGIN
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2001 Col=18 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-coli DH10B"

Query Match 75.0%; Score 15; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
|||||
Db 506 CGCTTCGATGAACCC 520

RESULT 8
TA140G03P 537 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 140g03, forward sequence, genomic survey sequence.
ACCESSION AL466454
VERSION AL466454.1 GI:11835809
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

REFERENCE
AUTHORS 1 (bases 1 to 537)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nhl@sanger.ac.uk

COMMENT
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@ligr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
SOURCE
1. 537
Location/Qualifiers

BASE COUNT
108 a 120 c 110 g 199 t
ORIGIN
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="140g03"

Query Match 75.0%; Score 15; DB 12; Length 537;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaac 18
|||||
Db 85 GGCCTTCGATGAAC 99

RESULT 9
TA190A10P/c 540 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 190a10, forward sequence, genomic survey sequence.
ACCESSION AL477985
VERSION AL477985.1 GI:11841795
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 540)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (4 kb). The v + 1 method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: neisayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at <http://www.sanger.ac.uk/projects/T-brucei/>.
FEATURES
source Location/Qualifiers
1..540
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="190a10"
BASE COUNT 177 a 118 c 126 g 119 t
ORIGIN
Query Match 75.0%; Score 15; DB 12; Length 540;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 ggcgttcgatgaac 18
|||||
DB 325 GCGCTTCGATGAC 311
RESULT 10
BH615799 631 bp DNA linear GSS 28-JAN-2002
LOCUS BMAC304F01SP6_P5U Brugia malayi Genomic Bac Library 3 Brugia
DEFINITION malayi genomic, DNA sequence.
ACCESSION BH615799
VERSION BH615799.1 GI:18380487
KEYWORDS GSS.
SOURCE Brugia malayi.
ORGANISM Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spturida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 631)
Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
J., Gilliano, D., Statko, B. and Blaxter, M.
Genome survey sequences from the human parasitic nematode Brugia
malayi
JOURNAL Unpublished (2000)
COMMENT Contact: Blaxter M.
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JF, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@sanger.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
Edinburgh, UK.
Seq primer: SP6 (ATTAGGTGACTATAG)
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..631
/organism="Brugia malayi"
/strain="TRS"
/db_xref="taxon:6279"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size ~48 kbp. The library was constructed by Claire
Whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
BASE COUNT 196 a 94 c 142 g 199 t
ORIGIN
Query Match 75.0%; Score 15; DB 12; Length 631;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 2 acggcgcttcgatga 16
|||||
DB 606 ACGGCGTTGATGA 620
RESULT 11
BE053145 690 bp mRNA linear EST 07-MAR-2001
LOCUS GA_Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
DEFINITION arboreum cDNA clone GA_Ea0002K16f, mRNA sequence.
ACCESSION BE053145
VERSION BE053145.2 GI:13244065
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosoids II; Malvales; Malvaceae; Gossypium.
1 (bases 1 to 690)
Wing, R.A., Frisch, D., Yu, Y., Malo, D., Rambo, T., Simmons, J., Henry
D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT On Jun 8, 2000 this sequence version replaced g1:8380201.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TATACGACTCCTATAGG
High quality sequence stop: 550.
FEATURES
source Location/Qualifiers
1..690
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0002K16f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/note="Vector: pRK-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 169 a 132 c 151 g 236 t
ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 690;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaac 18
 |||
 Db 567 GGCCTTCGATGAAC 581

RESULT 12
 CENS040Y/C 1033 bp DNA linear GSS 18-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 073004 of library G from Tetraodon nigroviridis, genomic survey
 sequence.

ACCESSION AL269530.1 GI:7991421
 VERSION AL269530
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 Tetraodontidae; Tetraodon.

REFERENCE 1 (bases 1 to 1033)
 AUTHORS Roest-Crollius,H., Jallou,O., Dasilva,C., Fitzames,C., Fisher,C.,
 Bouneau,L., Billaule,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1033)
 AUTHORS Roest-Crollius,H., Jallou,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzames,C., Wincker,P., Brotlier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 TITLE Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1033)
 AUTHORS Genoscope.

JOURNAL Direct Submission
 AUTHORS Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/Tetraodon.

FEATURES
 Location/Qualifiers

1..1033
 /organism="Tetraodon nigroviridis"

/db_xref="taxon:99883"

/clone="073004"

/clone_lib="G"

BASE COUNT 270 a 222 c 276 g 261 t 4 others
 ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 1033;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 cggcgttcgatgaac 17
 |||
 Db 460 CGCGCTTCGATGAA 446

RESULT 13
 BM007170 1218 bp mRNA linear EST 30-OCT-2001
 LOCUS 60361493371 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5420616 3',
 DEFINITION mRNA sequence.
 COMMENT BM007170

VERSION BM007170.1 GI:16521524
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1218)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs@email.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LCM1876 row: a column: 09
 High quality sequence start: 25
 High quality sequence stop: 313.

FEATURES
 Location/Qualifiers

1..1218
 /organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5420816"

/clone_lib="NIH_MGC_110"

/tissue_type="ductal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pOTB7; Site:1: XhoI;
 Site:2: EcoRI; CDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAC(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: This is a NIH_MGC Library."

BASE COUNT 370 a 446 c 244 g 154 t 4 others
 ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 1218;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
 |||
 Db 364 CGTTTCGATGAACC 378

RESULT 14
 AV640031 247 bp mRNA linear EST 15-DEC-2000
 LOCUS AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
 DEFINITION cDNA clone HCL009B04_r 5', mRNA sequence.
 ACCESSION AV640031 GI:10783359
 VERSION AV640031.1
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii.
 ORGANISM Chlamydomonas reinhardtii
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 247)
 AUTHORS Asamizu,E., Miura,K., Kucho,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
 Nakamura,Y. and Tabata,S.
 TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
 adapted cells of Chlamydomonas reinhardtii
 JOURNAL DNA Res. 7 (5), 305-307 (2000)
 MEDLINE 20539644
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
Source Location/Qualifiers

1. 247
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="HCL024a01.r"
/clone_jlb="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon dioxide"

BASE COUNT 61 a 79 c 54 g 53 t
ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 247;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
|||||
DB 245 GCGTTTCGATGAA 232

RESULT 15

AV640876 269 bp mRNA linear EST 15-DEC-2000
LOCUS AV640876 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
DEFINITION CDNA clone HCL024a01_r 5', mRNA sequence.
ACCESSION AV640876
VERSION AV640876.1 GI:10784204
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 269)
AUTHORS Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644

COMMENT Contact: Erika Asamizu

The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
Source Location/Qualifiers

1. 269
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="HCL024a01.r"
/clone_jlb="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; The cDNA library was constructed from cells cultured in a medium with bubbling air containing 5% carbon dioxide"

BASE COUNT 65 a 85 c 60 g 59 t
ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
|||||
DB 254 GCGTTTCGATGAA 241

Search completed: August 7, 2002, 23:12:33
Job time: 11072 sec

```
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (streptomycin), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match          100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
   ||||||||||||||||
Db 1 tacggcgcttcgatgaacc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA: 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
XX ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R.
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
XX tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
```

```
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (streptomycin), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match          100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgcttcgatgaacc 20
   ||||||||||||||||
Db 1 tacggcgcttcgatgaacc 20

RESULT 3
AAQ61457/c
ID AAQ61457 standard; DNA: 432 BP.
XX
AC AAQ61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M. tuberculosis rpoB gene fragment.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
XX mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
XX
PR 30-APR-1992; 92US-0875940.
XX
PR 14-AUG-1992; 92US-0929206.
XX
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASST-) ASSISTANCE PUBLIQUE.
XX
PA (INSP) INST PASTEUR.
XX
PA (MEDT-) MEDICAL RES COUNCIL.
XX
PA (UYBE-) UNIV BERNE.
XX
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
XX Young D, Zhang Y;
XX
DR WPI: 1993-368812/46.
XX
DR P-PSDB; AAR51372.
XX
```

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
PS Example 2: Fig 13: 97pp: English.
XX
XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M. tuberculosis (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgattgaacc 20
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAAA9863/C
ID AAA49863 standard; DNA; 480 BP.
XX
XX AAA49863;
AC
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key location/Qualifiers
FT primer_bind complement(41..60)
FT /*tag= a
FT /*note= "primer of AAA49823"
FT 372..391
FT /*tag= b
FT /*note= "primer of AAA49824"
ET
XX
XX WO200036142-A1.
PN
XX
XX 22-JUN-2000.
PD
XX
XX 10-DEC-1999; 99WO-CA01177.
PF
XX
XX 11-DEC-1998; 98US-0111794.
PR
XX
XX (VISI-) VISIBLE GENETICS INC.
PA
XX
XX Shipman R;
PI
XX
XX WPI; 2000-431611/37.
DR
XX
XX Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
PS
XX
XX Disclosure; Page 5; 43pp: English.
XX
XX The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgattgaacc 20
DB 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/C
ID AAT29126 standard; DNA; 620 BP.
XX
XX AAT29126;
AC
XX
DT 02-DEC-1996 (first entry)
XX
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KM Staphylococcus; identification; detection; ds.
XX
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO9615267-A1.
PN
XX
XX 23-MAY-1996.
PD
XX
XX 09-NOV-1995; 95WO-US14673.
PF
XX
XX 30-AUG-1995; 95US-0520946.
PR
XX
XX 09-NOV-1994; 94US-0337164.
PR
XX
XX 09-MAR-1995; 95US-0402601.
PR
XX
XX 07-JUN-1995; 95US-0484956.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
PI
XX
XX WPI; 1996-259862/26.
DR
XX
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
XX
XX Example 33; Page 306; 433pp: English.
PS
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (Rmw) RN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC R1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC amplified is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

SO Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACC 277

RESULT 6
AAT29124/C
ID AAT29124 standard; DNA; 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from Mycobacterium tuberculosis.
XX
KM P53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KM Staphylococcus; Identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN W09615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC amplified is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

SO Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACC 277

RESULT 7
AAT29125/C
ID AAT29125 standard; DNA; 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KM P53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
KM Staphylococcus; Identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN W09615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are


```

RESULT 9
AAH51976/C
ID AAH51976 standard; DNA: 3519 BP.
XX
XX AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KM Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI: 2001-329193/34.
DR P-PSDB; AAG81125.
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
PS Disclosure: Page 68-69; 207pp; English.
XX
XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
SQ Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;

```

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Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 1 tacgagcttcgatgaacc 20
   ||||||||||||||||
DB 1529 TACGGCGTTTCGATGAACCC 1510

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```

RESULT 10
AAH02079/C
ID AAH02079 standard; DNA: 3534 BP.
XX
XX AAH02079;
XX
XX 24-JUL-2001 (first entry)

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XX
XX Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
DE
XX
XX Species specific; genus specific; family specific; probe; detection;
KM identification; algal; archaeal; bacterial; fungal; parasitical;
KM microorganism; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial;
KM vaccine; primer; ds.
XX
XX
OS Mycobacterium tuberculosis.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
XX WPI: 2001-245006/25.
XX
XX Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitical species in a test sample -
XX
PS Disclosure: Page 1478-1479; 1580pp; English.
XX
XX The present invention describes a method for generating a repertoire of
CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitical species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexA nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella coli,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX which are given in the exemplification of the present invention.

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```

SQ Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;

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Query Match 100.0%; Score 20; DB 22; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 tacgagcttcgatgaacc 20
   ||||||||||||||||
DB 1547 TACGGCGTTTCGATGAACCC 1528

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RESULT 11

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AAA74651/C
ID AAA74651 standard; DNA; 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
KM rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PT particularly for detecting rifampin resistance in Mycobacterium
PT tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgattcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 12
ID AAA89994 standard; DNA; 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KM RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX

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PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PR 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PT Mycobacterium, comprising detecting mutations in a gene and relating
PT them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

```

```

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgattcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 13
ID AAT12096 standard; DNA; 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic; resistance; spectrum; gene; mycobacterium;
KM determination; amplification; tuberculosis; rpoB; fragment;
KM primer; differential; hybridisation; pattern; rifampicin;
KM rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machteldinckx L, Portael S;

```

```
PI Rosau R;
XX WPI: 1996-040250/04.
XX
XX Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
XX
XX Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;

Query Match          95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 19
   |||
Db 1 tacggcgttcgatgaacc 19

RESULT 14
AAT09670
ID AAT09670 standard; DNA; 27 BP.
XX
XX AAT09670;
XX
DT 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis 27-mer oligonucleotide DNA primer rpo397.
XX
KW Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Synthetic.
XX
PN W09533074-A1.
XX
PD 07-DEC-1995.
XX
PE 26-MAY-1995; 95WO-US06790.
XX
PR 26-MAY-1994; 94US-0250030.
XX
PA (HOFF ) HOFFMANN LA ROCHE INC.
PA (MAYO-) MAYO FOUNDATION.
XX
PI Feljmele TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
PI Young KKY;
XX
XX WPI: 1996-030581/03.
XX
PT Detection of Mycobacterium tuberculosis - by amplifying sample DNA
PT with a primer set that targets portions of the gene encoding rpoB.
XX
XX Claim 9; Page 39; 54pp; English.
XX
CC This oligonucleotide DNA primer is specific for Mycobacterium
CC tuberculosis, and may be used to amplify a sample DNA by targeting
CC a portion of the gene encoding rpoB. The method provides for the
```

```
CC detection of M. tuberculosis and the concurrent determination of its
CC drug susceptibility, particularly to rifampicin. The method can
CC provide often greater than 95% sensitivity and 100% specificity.
CC The biological sample is a fluid or tissue sample from a human.
XX
SQ Sequence 27 BP; 6 A; 7 C; 8 G; 6 T; 0 other;

Query Match          75.0%; Score 15; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaacc 20
   |||
Db 1 cgttcgatgaacc 15

RESULT 15
AAQ51532/c
ID AAQ51532 standard; DNA; 3447 BP.
XX
XX AAQ51532;
XX
DT 17-MAY-1994 (first entry)
XX
DE M.leprae rpoB gene.
XX
KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
XX Mycobacterium leprae.
XX
OS
XX
FH Key Location/Qualifiers
FT 1..3447 /*tag= a
FT CDS /note= "rifampicin-sensitive; in resistant
FT strains the Ser codon (TCG at
FT nucleotides 1273-1275) is often mutated
FT to a Phe, Met or esp. Leu codon"
XX
PN W09322454-A.
XX
PD 11-NOV-1993.
XX
PE 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP ) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UTBE-) UNIV BERNE.
PA (UTPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
XX WPI: 1993-368812/46.
XX
DR P-PSDB; AAR43671.
XX
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Fig 12; 97pp; English.
XX
CC PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium leprae strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AAQ51532) revealed
CC mutations in the region encoding amino acids 400-450. A common
```

CC mutation seen in resistant strains occurs at codon 425 where Ser is
 CC substituted, most frequently by Leu.
 XX
 SQ Sequence 3447 BP: 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 70.0%; Score 14; DB 14; Length 3447;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gttcgaatgaacc 20
 |||||
 DB 1448 GTTCGATGAACCC 1435

Search completed: August 8, 2002, 00:01:22
 Job time: 7611 sec

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CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC amplified is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

SO Sequence 620 BP: 103 A: 201 C: 214 G: 102 T: 0 other:

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA: 620 BP.

XX AAT29124;

DT 02-DEC-1996 (first entry)

DE rpoB gene fragment from Mycobacterium tuberculosis.

XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
XX Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
XX Staphylococcus; identification; detection; ds.

XX Mycobacterium tuberculosis.

XX WO9615267-A1.

XX 23-MAY-1996.

XX 09-NOV-1995; 95WO-US14673.

XX 30-AUG-1995; 95US-0520946.

XX 09-NOV-1994; 94US-0337164.

XX 09-MAR-1995; 95US-0402601.

XX 07-JUN-1995; 95US-0484956.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
XX Oldenburg MC, Olive DM;

XX WPI: 1996-259862/26.

XX Cleavage of nucleic acids to detect mutation(s) - allows detection
XX esp. in human p53 gene, to identify strains of microorganisms and
XX viruses

XX Example 33; Page 305; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease
XX selected from the group consisting of Cleavage (RTM) BN enzyme,
XX Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
XX polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
XX RadI/Rad10 complex. The nucleic acid substrate is preferably an
XX oligonucleotide containing a human p53 gene sequence or
XX alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

SO Sequence 620 BP: 103 A: 202 C: 214 G: 101 T: 0 other:

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. NO. 0.0073;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA: 620 BP.

XX AAT29125;

DT 02-DEC-1996 (first entry)

DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.

XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
XX Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
XX Staphylococcus; identification; detection; ds.

XX Mycobacterium tuberculosis.

XX WO9615267-A1.

XX 23-MAY-1996.

XX 09-NOV-1995; 95WO-US14673.

XX 30-AUG-1995; 95US-0520946.

XX 09-NOV-1994; 94US-0337164.

XX 09-MAR-1995; 95US-0402601.

XX 07-JUN-1995; 95US-0484956.

XX (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
XX Oldenburg MC, Olive DM;

XX WPI: 1996-259862/26.

XX Cleavage of nucleic acids to detect mutation(s) - allows detection
XX esp. in human p53 gene, to identify strains of microorganisms and
XX viruses

XX Example 33; Page 305-306; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease
XX selected from the group consisting of Cleavage (RTM) BN enzyme,
XX Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
XX polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
XX RadI/Rad10 complex. The nucleic acid substrate is preferably an
XX oligonucleotide containing a human p53 gene sequence or
XX alternatively, microbial gene sequences. Cleavage products are

PT Rapid detection of antibiotic resistance in *Mycobacteria* - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in *katG*, *rpoB* or *rpsL* genes
XX
PS Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain *rpoB* genes from rifampicin-
CC resistant *Mycobacterium leprae* strains. A comparison with the
CC sequence of the *rpoB* gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from *M. tuberculosis* (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.0076;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCCTTCGATGAACCC 409

RESULT 4

AAA49863/c standard; DNA; 480 BP.

AC AAA49863;

DT 25-SEP-2000 (first entry)

DE *Mycobacterium tuberculosis rpoB* gene (rifampin resistance).

KW Antibiotic resistance; *rpoB* gene; rifampin resistance; ss.

OS *Mycobacterium tuberculosis*.

FN Key Location/Qualifiers

FT primer_bind /tag= a complement(41..60)

FT primer_bind /note= "primer of AAA49823"

FT primer_bind /tag= b 372..391

FT primer_bind /note= "primer of AAA49824"

PN WO200036142-A1.

PD 22-JUN-2000.

PF 10-DEC-1999; 99WO-CA01177.

PR 11-DEC-1998; 98US-0111794.

PA (VISI-) VISIBLE GENETICS INC.

PI Shipman R;

DR WPI; 2000-431611/37.

PT Method for the detection and characterization of *Mycobacterium*

PT tuberculosis with antibiotic resistance in a sample -

XX Disclosure; Page 5; 43pp; English.

XX The present sequence is that of the *Mycobacterium tuberculosis*

CC *rpoB* (rifampin resistance) gene (bp2161-2640). Amplification and

CC cycle sequencing primers (see AAA49823-62) are used for the detection

CC and analysis of antibiotic resistance-associated mutations in

CC defined regions of *rpoB* (rifampin), *katG* (isoniazid), *oxyR-aphC* PR

CC (isoniazid), *mabA* (isoniazid), *rpsL/s12* (streptomycin), *16S/rrs*

CC (streptomycin), *embB* (ethambutol), *pncA* (pyrazinamide), *gyrA*
CC (ciprofloxacin) and *23S* (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC tuberculosis, and if present to evaluate the *rpoB*, *katG*, *rpsL/s12*
CC and *23S* genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.0075;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgttcgatgaacc 20
|||||
Db 451 TACGGCCTTCGATGAACCC 432

RESULT 5

AAT29126/c standard; DNA; 620 BP.

AC AAT29126;

DT 02-DEC-1996 (first entry)

DE *rpoB* gene fragment (mutant) from *Mycobacterium tuberculosis*.

KW p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;

KW Escherichia; Saccharomyces; Campylobacter; *Mycobacterium*; Shigella;

KW Staphylococcus; identification; detection; ds.

OS *Mycobacterium tuberculosis*.

FN WO9615267-A1.

PD 23-MAY-1996.

PF 09-NOV-1995; 95WO-US14673.

PR 30-AUG-1995; 95US-0520946.

PR 09-NOV-1994; 94US-0337164.

PR 09-MAR-1995; 95US-0402601.

PR 07-JUN-1995; 95US-0484956.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichnev VI;

PI Oldenburg MC, Olive DM;

DR WPI; 1996-259862/26.

PT Cleavage of nucleic acids to detect mutation(s) - allows detection

PT esp. in human p53 gene, to identify strains of microorganisms and

PT viruses

XX Example 33; Page 306; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease

CC selected from the group consisting of Cleavage (RTM) BN enzyme,

CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA

CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae

CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an

CC oligonucleotide containing a human p53 gene sequence or

CC alternatively, microbial gene sequences. Cleavage products are


```
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp
CC 2611-2592). It is used with the forward primer given in AAA49823
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), embA (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
   ||||||||||||||||
DB 1 tacggcgcttcgatgaacc 20

RESULT 2
AAA49826
ID AAA49826 standard; DNA: 20 BP.
XX
AC AAA49826;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KM ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI; 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
```

```
CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp
CC 2611-2592). It is used with the forward primer given in AAA49825 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embA (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match      100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0095;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
   ||||||||||||||||
DB 1 tacggcgcttcgatgaacc 20

RESULT 3
AAO61457/C
ID AAO61457 standard; DNA: 432 BP.
XX
AC AAO61457;
XX
DT 17-MAY-1994 (first entry)
XX
DE M. tuberculosis rpoB gene fragment.
XX
KM rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO9322454-A.
XX
PD 11-NOV-1993.
XX
PF 30-APR-1993; 93WO-EP01063.
XX
PR 17-SEP-1992; 92FR-0011098.
PR 30-APR-1992; 92US-0875940.
PR 14-AUG-1992; 92US-0929206.
PR 16-APR-1993; 93FR-0004545.
XX
PA (ASSI-) ASSISTANCE PUBLIQUE.
PA (INSP-) INST PASTEUR.
PA (MEDI-) MEDICAL RES COUNCIL.
PA (UYBE-) UNIV BERNE.
PA (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
DR WPI; 1993-368812/46.
DR P-PSDB; AAR51372.
XX
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:25 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: us-09-786-105-4

Perfect score: 20
Sequence: 1 tacggcgcttcgatgaacc 20

Scoring table:

OLIGO_NUC
Gap 60.0 , Gapext 60.0

Searched: 1736436 segs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	21	AAA49824
2	20	100.0	20	21	AAA49826
3	20	100.0	432	14	AAO61457
4	20	100.0	480	21	AAA49863
5	20	100.0	620	17	AAAT29126
6	20	100.0	620	17	AAAT29124
7	20	100.0	620	17	AAAT29125
8	20	100.0	970	17	AAAT09676
9	20	100.0	3519	22	AAH51976

C	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
C	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
C	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
C	13	19	95.0	19	17	AAAT12096	M. tuberculosis rp
C	14	15	75.0	27	17	AAAT09670	Mycobacterium tube
C	15	14	70.0	3447	14	AAO51532	M. leprae rpoB gene
C	16	14	70.0	3474	23	AAAS1357	Enterococcus faeca
C	17	14	70.0	3624	23	AAAS2892	Enterococcus faeca
C	18	14	70.0	6275	24	ABL22551	Human Immune syste
C	19	14	70.0	6319	23	ABL18447	Drosophila melanog
C	20	14	70.0	9179	20	AAAX13246	Enterococcus faeca
C	21	14	70.0	9728	24	ABL33903	Human Immune syste
C	22	14	70.0	29555	23	ABL38446	Drosophila melanog
C	23	13	65.0	58	22	AAAF61643	Lactobacillus case
C	24	13	65.0	234	17	AAAT13651	ACNPV ORF 43, res1
C	25	13	65.0	351	22	AAAF1558	Lactobacillus case
C	26	13	65.0	383	19	AAV04618	Flea aminopeptidas
C	27	13	65.0	383	22	AAAC9090	Flea aminopeptidas
C	28	13	65.0	421	23	AAAS94185	DNA encoding novel
C	29	13	65.0	537	19	AAV04619	DNA encoding novel
C	30	13	65.0	537	22	AAAC90901	Flea aminopeptidas
C	31	13	65.0	667	22	AAAF1326	Corynebacterium gl
C	32	13	65.0	1086	22	AAAF27618	Mevalonate pathway
C	33	13	65.0	1227	23	AAAS87269	Drosophila melanog
C	34	13	65.0	1242	23	ABL22843	Staphylococcus aur
C	35	13	65.0	1261	18	AAV74720	C glutamicum codin
C	36	13	65.0	1326	22	AAH68314	S. epidermidis ope
C	37	13	65.0	1407	22	AAH53127	Arabidopsis thaila
C	38	13	65.0	1473	21	AAAC8699	Murine FARP1 codin
C	39	13	65.0	1475	21	AAAC32775	DNA encoding novel
C	40	13	65.0	1938	22	AAAF89013	DNA encoding novel
C	41	13	65.0	2109	23	AAAS92952	Human FATP variant
C	42	13	65.0	2192	23	AAAS92789	DNA encoding novel
C	43	13	65.0	2222	20	AAAS38124	Drosophila melanog
C	44	13	65.0	2470	23	AAAS94186	
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ALIGNMENTS

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XX	XX
AC	AAA49824;
XX	XX
DT	25-SEP-2000 (first entry)
XX	XX
DE	Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.
XX	XX
KW	Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW	ss.
XX	XX
OS	Mycobacterium tuberculosis.
XX	XX
PN	WO200036142-A1.
XX	XX
PD	22-JUN-2000.
XX	XX
PF	10-DEC-1999; 99WO-COA01177.
XX	XX
PR	11-DEC-1998; 98US-O111794.
XX	XX
PA	(VIST-) VISIBLE GENETICS INC.
PI	Shipman R;
XX	XX
DR	WPI; 2000-431611/37.
XX	XX
PT	Method for the detection and characterization of Mycobacterium
PT	tuberculosis with antibiotic resistance in a sample -
XX	XX

Thu Aug 8 09:35:17 2002

us-09-786-105-4.oli.rge

Page 8


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ORIGIN

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Best Local Similarity	100.0%	Pred. No. 0.058;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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VERSION	AE006964 AE000516
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SOURCE	Mycobacterium tuberculosis CDC1551.
ORGANISM	Mycobacterium tuberculosis CDC1551

REFERENCE 1 (bases 1 to 19352)

TITLE	Whole genome comparison of <i>Mycobacterium tuberculosis</i> clinical and laboratory strains
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 19352)
AUTHORS	Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O.,

TITLE Direct Submission
JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA

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gene
CDS

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CDS      complement(7691.  .8065)

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Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taagcgcttcgatgaacc 20
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Db 1547 TACGGCGTTTCGATGAACC 1528

RESULT 13
MTU12205/c 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.

ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE
ORGANISM Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 3853)
AUTHORS Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNML Unpublished
REFERENCE 2 (bases 1 to 3853)
AUTHORS Imboden, P.
TITLE Direct Submission
JOURNML Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland

FEATURES

source Location/Qualifiers
1. 3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
576..>3853
/gene="rpoB"
/codon_start=1
/transl_table=1
/product="RNA polymerase beta subunit"
/protein_id="AAA20242.2"
/db_xref="GI:714499"

/translation="MEGCILADSRQSKTAASPSRPOSSNNNSVPGAPNRVSFAKL
REPLEVGLDVQTDSEFMILGSPRMSAERDVPVGLLEVLLELPIDFSGS
MSLSFSDPRDDVKAPEYDECKDKMTAAFLPYAEIINNNGEIKSQYPMGDFPM
TEKGTFLINGTERVVSOLVRSPEVYDETDIDTSKTLNKKYIPRSGAMLEVDVK
RDYGVADIDRRKRPVTVLKAIGMTSEQIVERRGSEIMKSTLEKNTGTDEALLD
IYKLRPGEPTKESAOITLLENLFKERYDLAVGRYKVKRKLGLHVGEPITSTLT
EEDVVAITIEVLRLHEGQITMTYVGGVEVETDDIDHFGNRLRTYVGEILIONIRVG
MSRMRVRRMTQDVEAITPOTLINIRPVAAIKFEGTSOLQSPMDONNPLSGIT
HKRLSALGCGLSRERAGLEVHVHSHGRMCPITTPGPNIGLIGLSISVAVRVP
EGTEPTPRKRVVDSVSDGIVTLADEEDRHVAQAANPIDADGRFVEPVVLRKRG
EVEYPSSEVDYVDSRQVAVATAMTPELEHDAARALMAGMOKQAVPLVSEAP
LVGEMELRAIDAATSSSOESGVIEVSADYITVMINDGTRTRYRMRKPARSHGTC
ANOCPIVDADRVAGQVADGCTDDEMALGKNLVAIMPENGHYEDAILISNLT
VEEDVVAITIEEHEIDARDTKGAIEITRDIPNISDEVLADDERGIVRIGAVRG
DIYGVKTPKGETELPEERLRAIFEKARREVDITSLKVPHGSGKVIIGIVRSRD
EDELPAVNELVRYVAOKRKISDGLAHRGKVGIGKILPEYEDPFLADGPVUI
ILNTHGVPRRMNTGQILIEHLGMAHSGMVDAAKGVDMARLPDELLAQNPAVTS
TPVFDGAQEAELQGLSTCLPNRGDVLVDADGAKMLFDRSGEPPEPYPTVGYMYIM
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BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.057;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 taagcgcttcgatgaacc 20
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Db 2122 TACGGCGTTTCGATGAACC 2103

RESULT 14
MSGRPOB/c 5084 bp DNA linear BCT 13-SEP-1994
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
DEFINITION gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
partial cds.

ACCESSION L27989
VERSION L27989.1 GI:468333
KEYWORDS RNA polymerase beta-subunit; rpoB gene.
SOURCE Mycobacterium tuberculosis (strain RV) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 5084)
AUTHORS Miller, L.P., Crawford, J.T. and Shinnick, T.M.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNML Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
MEDLINE 94304130

FEATURES

source Location/Qualifiers
1. 5084
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/db_xref="taxon:1773"
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/evidence="experimental"
/product="RNA polymerase beta'-subunit"
/protein_id="AAA21417.1"
/db_xref="GI:468334"

/translation="MEGCILADSRQSKTAASPSRPOSSNNNSVPGAPNRVSFAKL
REPLEVGLDVQTDSEFMILGSPRMSAERDVPVGLLEVLLELPIDFSGS
MSLSFSDPRDDVKAPEYDECKDKMTAAFLPYAEIINNNGEIKSQYPMGDFPM
TEKGTFLINGTERVVSOLVRSPEVYDETDIDTSKTLNKKYIPRSGAMLEVDVK
RDYGVADIDRRKRPVTVLKAIGMTSEQIVERRGSEIMKSTLEKNTGTDEALLD
IYKLRPGEPTKESAOITLLENLFKERYDLAVGRYKVKRKLGLHVGEPITSTLT
EEDVVAITIEVLRLHEGQITMTYVGGVEVETDDIDHFGNRLRTYVGEILIONIRVG
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LVGEMELRAIDAATSSSOESGVIEVSADYITVMINDGTRTRYRMRKPARSHGTC
ANOCPIVDADRVAGQVADGCTDDEMALGKNLVAIMPENGHYEDAILISNLT
VEEDVVAITIEEHEIDARDTKGAIEITRDIPNISDEVLADDERGIVRIGAVRG
DIYGVKTPKGETELPEERLRAIFEKARREVDITSLKVPHGSGKVIIGIVRSRD
EDELPAVNELVRYVAOKRKISDGLAHRGKVGIGKILPEYEDPFLADGPVUI
ILNTHGVPRRMNTGQILIEHLGMAHSGMVDAAKGVDMARLPDELLAQNPAVTS
TPVFDGAQEAELQGLSTCLPNRGDVLVDADGAKMLFDRSGEPPEPYPTVGYMYIM
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TIKS"

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4641..>5084
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/product="RNA polymerase beta'-subunit"
/protein_id="AAA21417.1"
/db_xref="GI:537608"

partial cds.
AF060353
VERSION AF060353.1 GI:3133464
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 705)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
MEDLINE 9824865
REFERENCE 2 (bases 1 to 705)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (20-APR-1998) Division of Infectious Disease, Affimetrix,
380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
source
1. 705
/organism="Mycobacterium tuberculosis"
/strain="ATCC27294"
/db_xref="ATCC:27294"
/db_xref="taxon:11773"
<1. >705
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/product="RNA polymerase beta-subunit"
/protein_id="AC38533.1"
/db_xref="GI:3133465"
/translation="ODVEATTPQTLINIRPVNAIKFEFTSOLSDPMDONPLSGLT
HKRRISLIGCGISREPRAGLEVDVHSHGRCPIETPGSPINGLIGSSVYARVP
FGERTPIYRKVGVGVSDVETVLTADDEDDHYVAQANSPIDAQGRPEPVYLRKRG
EVEIVPSVEDVMDVSPROMSVATAMIPLEHDDANLGMAMORQAVPLVRSSEAP
LVGTGMLRAIDAAT"
BASE COUNT 117 a 227 c 250 g 111 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 331 TACGGCGTTTCGATGAACCC 312
RESULT 10
ARI49128/c ARI49128 706 bp DNA linear PAT 08-AUG-2001
LOCUS
DEFINITION Sequence 24 from patent US 6228575.
ACCESSION ARI49128
VERSION ARI49128.1 GI:15113719
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 706)
AUTHORS Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
Ghandour,G. and Wang,C.
TITLE Chip-based species identification and phenotypic characterization
of microorganisms
JOURNAL Patent: US 6228575-A 24 08-MAY-2001;
FEATURES
Location/Qualifiers

source 1. 706
/organism="unknown"
BASE COUNT 117 a 227 c 250 g 111 t 1 others
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcggttcgatgaacc 20
Db 332 TACGGCGTTTCGATGAACCC 313
RESULT 11
I50706/c I50706 970 bp DNA linear PAT 07-OCT-1997
LOCUS
DEFINITION Sequence 1 from patent US 5643723.
ACCESSION I50706
VERSION I50706.1 GI:2472409
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 970)
AUTHORS Persing,D.H., Hunt,J.J., Young,K.K.Y., Fellmlee,T.A., Roberts,G.D.
and Whelan,A.Christian.
TITLE Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
JOURNAL Patent: US 5643723-A 1 01-JUL-1997;
FEATURES
source
1. 970
/organism="unknown"
BASE COUNT 182 a 302 c 330 g 156 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcggttcgatgaacc 20
Db 671 TACGGCGTTTCGATGAACCC 652
RESULT 12
AX111339/c AX111339 3534 bp DNA linear PAT 30-APR-2001
LOCUS
DEFINITION Sequence 2072 from Patent WO0123604.
ACCESSION AX111339
VERSION AX111339.1 GI:13927631
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteriia; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 3534)
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2072 05-APR-2001;
FEATURES
source
1. 3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
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DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c AR062058 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 137 from patent US 5843669.
DEFINITION AR062058
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL jannaschii FEN-1 endonucleases
FEATURES Patent: US 5843669-A 137 01-DEC-1998;
Source 1..620
/organism="unknown"

BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059 AR062059 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 138 from patent US 5843669.
DEFINITION AR062059
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL jannaschii FEN-1 endonucleases
FEATURES Patent: US 5843669-A 138 01-DEC-1998;
Source 1..620
Location/Qualifiers

BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
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DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060 AR062060 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 139 from patent US 5843669.
DEFINITION AR062060
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL jannaschii FEN-1 endonucleases
FEATURES Patent: US 5843669-A 139 01-DEC-1998;
Source 1..620
Location/Qualifiers

BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
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DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061 AR062061 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 140 from patent US 5843669.
DEFINITION AR062061
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL jannaschii FEN-1 endonucleases
FEATURES Patent: US 5843669-A 140 01-DEC-1998;
Source 1..620
Location/Qualifiers

BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
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DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c AF060353 705 bp DNA linear BCT 15-MAY-1998
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,
DEFINITION

CDS

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/protein_id="AAB59068.1"
/db_xref="GI:149992"
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149
variation /phenotype="rifampicin resistant in association with
mutation 234 G"
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191 /replace="c"
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mutation 203 T"
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254 /replace="c"
BASE COUNT 77 a 140 c 148 g 67 t
ORIGIN

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
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Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
AR067448/c 432 bp DNA linear PAT 29-SEP-1999
LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
ACCESSION AR067448
VERSION AR067448.1 GI:5998670
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 432)
AUTHORS Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and Bodmer,T.
TITLE Rapid detection of antibiotic resistance in mycobacterium tuberculosis
JOURNAL Patent: US 5851763-A 59 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..432
BASE COUNT 77 a 139 c 149 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
AR062056/c 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062056
DEFINITION Sequence 135 from patent US 5843669.
ACCESSION AR062056
VERSION AR062056.1 GI:5989747
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus jannaschii FEN-1 endonucleases
JOURNAL Patent: US 5843669-A 135 01-DEC-1998;
FEATURES Location/Qualifiers
source 1..620
BASE COUNT 103 a 202 c 214 g 101 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
AR062057/c 620 bp DNA linear PAT 29-SEP-1999
LOCUS AR062057
DEFINITION Sequence 136 from patent US 5843669.
ACCESSION AR062057
VERSION AR062057.1 GI:5989748
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:49:03 ; Search time 2179.67 Seconds
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Title: US-09-786-105-4

Perfect score: 20
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Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
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6: gb_pat:*
7: gb_ph:*
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32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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C	1	20	100.0	432	1	MSGRIFFRNAP	L05910 Mycobacteri
C	2	20	100.0	432	6	AR067448	AR067448 Sequence
C	3	20	100.0	620	6	AR062056	AR062056 Sequence
C	4	20	100.0	620	6	AR062057	AR062057 Sequence
C	5	20	100.0	620	6	AR062058	AR062058 Sequence
C	6	20	100.0	620	6	AR062059	AR062059 Sequence
C	7	20	100.0	620	6	AR062060	AR062060 Sequence
C	8	20	100.0	620	6	AR062061	AR062061 Sequence
C	9	20	100.0	705	1	AF060353	AF060353 Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128 Sequence
C	11	20	100.0	970	6	I50706	I50706 Sequence 1
C	12	20	100.0	3534	6	AX111339	AX111339 Sequence
C	13	20	100.0	3853	1	MTU12205	MTU12205 Sequence
C	14	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
C	15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
C	16	20	100.0	19770	1	MTC1376	Z59972 Mycobacteri
C	17	17	85.0	3316	1	AF172323	AF172323 Bacillus
C	18	15	75.0	27	6	I50714	I50714 Sequence 9
C	19	15	75.0	11843	1	AE008100	AE008100 Agrobacte
C	20	15	75.0	13735	1	AE009134	AE009134 Agrobacte
C	21	15	75.0	239050	1	AL596169	AL596169 Listeria
C	22	14	70.0	143	3	AF277396	AF277396 Citrobact
C	23	14	70.0	409	1	CSPA622R	Z47191 Calothrix D
C	24	14	70.0	442	8	AF080428	AF080428 Agrocyste
C	25	14	70.0	458	1	AF080421	AF080421 Agrocyste
C	26	14	70.0	518	1	AF325874	AF325874 Staphyloc
C	27	14	70.0	762	1	SHEFWYC	MS3306 S. flexneri
C	28	14	70.0	791	33	AC048639	AC048639 Giardia 1
C	29	14	70.0	1128	8	AB044172	AB044172 Yamagishi
C	30	14	70.0	1194	3	FHEFHMDA	L36247 Fasciola he
C	31	14	70.0	1959	8	ATHTUBA6A	M84699 Arabidopsis
C	32	14	70.0	2612	3	FHEFHMDA	L36248 Fasciola he
C	33	14	70.0	2615	10	RNPKCEPA	X68400 R. norvegicu
C	34	14	70.0	3218	10	AF146518	AF146518 Rattus no
C	35	14	70.0	3240	8	SCU06465	U06465 Saccharomyc
C	36	14	70.0	3447	6	AR067447	AR067447 Sequence
C	37	14	70.0	3639	10	AF214568	AF214568 Rattus no
C	38	14	70.0	4075	38	AF146044	AF146044 Rattus no
C	39	14	70.0	4887	3	AY069181	AY069181 Drosophila
C	40	14	70.0	6211	3	CEFI1A5	Z75951 Caenorhabdi
C	41	14	70.0	6275	6	AX345453	AX345453 Sequence
C	42	14	70.0	6275	6	AX348335	AX348335 Sequence
C	43	14	70.0	9086	1	AE001767	AE001767 Thermotog
C	44	14	70.0	9728	6	AX346805	AX346805 Sequence
C	45	14	70.0	9728	6	AX348479	AX348479 Sequence

ALIGNMENTS

RESULT 1
MSGRIFFRNAP/c 432 bp DNA linear BCT 21-MAY-1993
LOCUS Mycobacterium tuberculosis RNA polymerase beta subunit, rifampicin
DEFINITION resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Antimicrob. Agents Chemother. 34(1, 647-650 (1993)
FEATURES
source Location/Qualifiers
1..432
/organism="Mycobacterium tuberculosis"
/strain="H37"

JOURNAL Genome Res. 10 (12), 2030-2043 (2000)
 MEDLINE 20568492
 COMMENT On Aug 17, 1999 this sequence version replaced gi:5735350.

Contact: Brian Oliver
 Laboratory of Cellular and Developmental Biology
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 6 Center Drive MSC 2715, Bldg 6, Rm BI-13, Bethesda, MD 20892 USA
 Fax: (301) 496 5239
 Email: oliverbhelix.nih.gov
<http://www.niddk.nih.gov/intram/people/boliver.htm>
 Tissue Isolation and Library construction performed at the National
 Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
<http://www.niddk.nih.gov/intram/people/boliver.htm>). DNA sequencing
 and analyses performed by National Institutes of Health Intramural
 Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
 Plate: 07 row: c column: 12
 Seq primer: M13R1 reverse primer (ABI).
 Location/Qualifiers

FEATURES

source

```
1..379
/organism="Drosophila melanogaster"
/strain="y[*] w[67c1]/Y"
/db_xref="taxon:7227"
/clone_lib="Ds07c12"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Stratagene)"
/note="Organ: testis; Vector: pBluescript SK (Stratagene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
day adult y[*] w[67c1]/Y males raised at 25°C. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using oligotex (Qiagen). cDNA
library constructed using Stratagene Zap-cDNA synthesis
kit. Oligo dT primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
```

BASE COUNT 104 a 96 c 113 g 66 t
 ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 379;
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 acggtcggcgagctg 16
 ||||||||||||
 Db 39 ACGGTCGGCGAGCTG 53

Search completed: August 7, 2002, 23:12:33
 Job time: 11072 sec

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RESULT 13
LOCUS BE423869/c 237 bp mRNA linear EST 24-JUL-2000
DEFINITION WHE0067_F05_K0925 wheat endosperm cDNA library Triticum aestivum
CDNA clone WHE0067_F05_K09, mRNA sequence.
ACCESSION BE423869
VERSION BE423869.1 GI:9421712
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1. Triticaceae; Triticum.
1 (bases 1 to 237)
Altenbach,S., Anderson,O.D., Chao,S., Gallil,G., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Endosperm cDNA library
Unpublished (2000)
JOURNAL Contact: Olin Anderson
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595723
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strataene SK primer.

FEATURES
Source
Location/Qualifiers
1..237
/organism="Triticum aestivum"
/cultivar="Cheyenne"
/db_xref="taxon:4565"
/clone="WHE0067_F05_K09"
/clone_lib="wheat endosperm cDNA library"
/rissue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli SOLR"
/Note="Vector: Lambda ZAP II, excised phagemid; Site_1:
EcoRI; Seeds collected, endosperm isolated, and RNA
prepared by Susan Altenbach. Library constructed by
Strataene, Inc. Plasmid DNA preparations and DNA
sequencing were performed in the OD Anderson lab."

BASE COUNT 65 a 79 c 40 g 53 t
ORIGIN

Query Match 75.0% Score 15; DB 10; Length 237;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 tcgcgcagctatcc 20
|||||
Db 79 TCGCGCAGCTGATCC 65

RESULT 14
LOCUS A1945868 376 bp mRNA linear EST 08-JAN-2001
DEFINITION bs17907.y1 Drosophila melanogaster adult testis library Drosophila
melanogaster cDNA clone bs17907 5', mRNA sequence.
ACCESSION A1945868
VERSION A1945868.2 GI:9991196
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 376)
Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and

```

```

TITLE Oliver,B.
JOURNAL Gene discovery using computational and microarray analysis of
DEFINITION transcription in the drosophila melanogaster testis
GENEID Genome Res. 10 (12), 2030-2043 (2000)
COMMENT 20568492
On Aug 17, 1999 this sequence version replaced gi:5736266.
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: oliver@helix.nih.gov,
http://www.niddd.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddd.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 17 row: 9 column: 07
Seq primer: M13RP1 reverse primer (ABI).

FEATURES
Source
Location/Qualifiers
1..376
/organism="Drosophila melanogaster"
/strain="Y[*] w[67c1]/Y"
/db_xref="taxon:7227"
/clone="bs17907"
/clone_lib="Drosophila melanogaster adult testis library"
/sex="male"
/dev_stage="1-5 day adult"
/lab_host="SOLR (Strataene)"
/Note="Organ: testis; Vector: pBluescript SK (Strataene);
Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
day adult Y[*] w[67c1]/Y males raised at 25°C. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Strataene ZAP-cDNA synthesis
kit. Oligo dt-primed, size fractionated -1.6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBluescript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

BASE COUNT 110 a 94 c 107 g 65 t
ORIGIN

Query Match 75.0% Score 15; DB 9; Length 376;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 acggtcgcgcagctg 16
|||||
Db 272 ACGGTCGCGCAGCTG 286

RESULT 15
LOCUS A1944952 379 bp mRNA linear EST 08-JAN-2001
DEFINITION bs07c12.y1 Drosophila melanogaster adult testis library Drosophila
melanogaster cDNA clone bs07c12 5', mRNA sequence.
ACCESSION A1944952
VERSION A1944952.2 GI:9990300
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 379)
Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and

```

Gene discovery using computational and microarray analysis of transcription in the drosophila melanogaster testis

FEATURES

Location/Qualifiers
1. 606

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone="5333151"

/clone_lib="zebrafish adult brain"

/sex="mixed male and female"

/tissue_type="brain"

/dev_stage="adult"

/lab_host="E. coli DH10B"

/note="Vector: pZiPlox; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaZiPlox. Mass excision of the cDNA library was performed to yield pZiPlox plasmids. Insert check was done in original library."

BASE COUNT

209 a 133 c 139 g 125 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 74; Length 606;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgtcgcgcagctg 16

Db 452 TACGTCGCAGCTG 437

RESULT 11
B1888442/c 640 bp mRNA linear EST 12-OCT-2001
LOCUS
DEFINITION B1888442 zebrafish shield stage whole embryo cDNA library
MPMGP637 Danio rerio cDNA clone MPMGP637_18E17;MPMGP637E1718 5',
mRNA sequence.
ACCESION B1888442.1 GI:16095713
VERSION
KEYWORDS
SOURCE
ORGANISM

Danio rerio.
zebrafish.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 640)
Clark, M., Anstad, P., Hennig, S., Johnson, S. L. and Lehrach, H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)

JOURNAL

Contact: Hennig S
laboratory 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
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Tel: +49 30 8413 1612
Fax: +49 30 8413 1360
Email: hennig@molgen.mpg.de

5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 640.

FEATURES

Location/Qualifiers
1. 640

/organism="Danio rerio"

/db_xref="taxon:7955"

/clone="MPMGP637_18E17;MPMGP637E1718"

/clone_lib="zebrafish shield stage whole embryo cDNA
library MPMGP637"

/tissue_type="whole embryo"

/dev_stage="shield stage, 6 hrs post-fertilisation"

/lab_host="E. coli, XLI blue MRF"

/note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
oligo-dt-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"

BASE COUNT

209 a 152 c 139 g 139 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 74; Length 640;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacgtcgcgcagctg 16

Db 541 TACGTCGCAGCTG 526

RESULT 12
BE585978 708 bp mRNA linear EST 17-AUG-2000
LOCUS
DEFINITION BE585978 A09_a9_065 KSU wheat Fusarium graminearum infected spike
cDNA library Triticum aestivum cDNA clone Est#7PT7_A09_a9_065, mRNA
sequence.
ACCESION BE585978
VERSION BE585978.1 GI:9839010
KEYWORDS
SOURCE
ORGANISM

bread wheat.
Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1 (bases 1 to 708)
Fellers, J. P., Li, W. L., Hill, Ambroz, K., Matthews, A. and Gill, B. S.
The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library
Unpublished (2000)

JOURNAL

Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@afalfa.ksu.edu
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: 77.

FEATURES

Location/Qualifiers
1. 708

/organism="Triticum aestivum"

/cultivar="Sumai3"

/db_xref="taxon:4565"

/clone="Est#7PT7_A09_a9_065"

/clone_lib="KSU wheat Fusarium graminearum infected spike
cDNA library"

/tissue_type="Spike"

/dev_stage="Adult Plant"

/lab_host="E. coli JM109"

/note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;
Plants were grown in the greenhouse. Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT

154 a 221 c 156 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 75; Length 708;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 gtccgcgcagctgctcc 20

Db 559 GTCCGCAGCTGATCC 574

ORIGIN

```

BASE COUNT      26 a      41 c      44 g      18 t      1 others
ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 130;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 gtcgcgcagctgattcc 20
      |||
Db      90 gtcgcgcagctgattcc 75

RESULT 8
LOCUS    BM396091      132 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM396091
VERSION   BM396091.1 GI:18196144
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 132)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
, J. and Klobutcher, L., 1992.
EST from Tetrahymena thermophila, strain C0428.1, growing cells
Unpublished (2002)
JOURNAL
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..132
/organism="Tetrahymena thermophila"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      27 a      42 c      44 g      19 t

ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 132;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 gtcgcgcagctgattcc 20
      |||
Db      92 gtcgcgcagctgattcc 77

RESULT 9
LOCUS    BM398255      134 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM398255
VERSION   BM398255.1 GI:18196308
KEYWORDS
SOURCE
ORGANISM
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

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REFERENCE
1 (bases 1 to 134)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
, J. and Klobutcher, L., 1992.
EST from Tetrahymena thermophila, strain C0428.1, growing cells
Unpublished (2002)
JOURNAL
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
1..134
/organism="Tetrahymena thermophila"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT      26 a      44 c      46 g      18 t

ORIGIN

Query Match      80.0%; Score 16; DB 10; Length 134;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      5 gtcgcgcagctgattcc 20
      |||
Db      94 gtcgcgcagctgattcc 79

RESULT 10
LOCUS    BI981973      606 bp      mRNA      linear      EST 24-OCT-2001
DEFINITION
BI981973 zebrafish adult brain Danio rerio cDNA clone 5333151 5'
similar to TR:Q9Y4D4 Q9Y4D4 KIA00648 PROTEIN ;, mRNA sequence.
ACCESSION
BI981973
VERSION   BI981973.1 GI:16371108
KEYWORDS
SOURCE
ORGANISM
Danio rerio
zebrafish.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 606)
Clark, M., Johnson, S.L., Lehnach, H., Lee, R., Li, F., Marra, M., Eddy
, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B.,
Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E.,
Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
and Wilson, R.
Washu zebrafish EST Project 1998
Unpublished (1998)
Other-ESTs: fu53f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzpd.de)
High quality sequence stop: 446.

```

/tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: lambda Uni-ZAP XR, excised phagemid
 Bluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close Lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give Bluescript phagemids before
 normalization library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 144 a 209 c 165 g 140 t
 ORIGIN
 Query Match 85.0%; Score 17; DB 10; Length 658;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgagctgattcc 20
 |||||||
 Db 512 GGTGCGGAGCTGATCC 528

RESULT 6 828 bp mRNA linear EST 17-OCT-2001
 LOCUS BM397722
 DEFINITION HVSME0021120f Hordeum vulgare seedling shoot EST library
 HVCNMA0001 (Cold stress) Hordeum vulgare cDNA clone HVSME0021120f,
 mRNA sequence.
 ACCESSION BM397722
 VERSION BM397722.1 GI:13087434
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Hordeum.
 1 (bases 1 to 828)
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Fritsch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
 Fenton, R.D. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex cold-stressed seedling shoot cDNA
 library
 Unpublished (2001)
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 574
 Seq primer: AATTAAACCTCAGCTAAGGG
 High quality sequence stop: 643.
 Location/Qualifiers
 1..828
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSME0021120f"
 /clone_1lb="Hordeum vulgare seedling shoot EST library
 HVCNMA0001 (Cold stress)"
 /tissue_type="Seedling shoot"

/lab_host="TJCl21"
 /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50c for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give Bluescript SK(-) cDNA
 phagemids. These steps were performed in the T7 Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Fritsch, Atkins and Wing). Plasmid DNA preparations
 , DNA sequencing and sequence analysis were performed at
 CUGI (Wing, Yu, Fritsch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders also
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t
 ORIGIN
 Query Match 85.0%; Score 17; DB 10; Length 828;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgagctgattcc 20
 |||||||
 Db 500 GGTGCGGAGCTGATCC 516

RESULT 7 130 bp mRNA linear EST 17-JAN-2002
 LOCUS BM397871
 DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM397871
 VERSION BM397871.1 GI:18197924
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila
 Eukaryote; Alveolata; Ciliophora; Oligohymenophorea;
 Hymenostomatida; Tetrahymenina; Tetrahymena.
 1 (bases 1 to 130)
 Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E., Frankel
 , J. and Klobutcher, L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 Contact: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apurkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..130
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_1lb="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript SK+; Details on library
 preparation can be found in Chilcoat and Turkewitz (2001)

surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and ceftaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the T₇ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pluscript phagemids before normalization library was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcgcgcgcgtgatcc 20
Db 514 ggtcgcgcgcgtgatcc 530

RESULT 4
BE195103 610 bp mRNA linear EST 22-OCT-2001
LOCUS HVSMH0088E21f Hordeum vulgare 5-45 DAP spike EST library
DEFINITION HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMH0088E21f, mRNA sequence.

ACCESSION BE195103
VERSION BE195103.3 GI:16321083
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Hordeum.
1 (bases 1 to 610)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.

COMMENT Contact: Wing RA
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu

JOURNAL Total hg bases = 238
Seq primer: AATTAACCTCCTCACTAAGG
High quality sequence stop: 563.

FEATURES
Source Location/Qualifiers
1..610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMH0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP)
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,

30 and 45 DAP (Fenton). Total RNA was prepared from each pool. Equal quantities of all six RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million p10 were in vivo excised to give pluscript SK(-) cDNA phagemids (Choi) in the T₇ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

BASE COUNT 127 a 203 c 158 g 120 t 2 others

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ggtcgcgcgcgtgatcc 20
Db 499 ggtcgcgcgcgtgatcc 515

RESULT 5
BE442518 658 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1101_H10_O19Zs wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1101_H10_O19, mRNA sequence.

ACCESSION BE442518
VERSION BE442518.1 GI:9442034
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae ; Triticeae; Triticum.
1 (bases 1 to 658)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov

JOURNAL

COMMENT Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stragagene SK primer.
Location/Qualifiers
1..658
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_O19"
/clone_lib="Wheat etiolated seedling root normalized cDNA library"

/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK, Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 84 a 130 c 124 g 84 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 gtcgcgcagctgattcc 20
|||||
Db 86 gtcgcgcagctgattcc 102

RESULT 2
BE445100 544 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1132_H08_P16ZS wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
sequence.
ACCESSION BE445100
VERSION BE445100.1 GI:9444655
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 544)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsiao,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
/clone_1lb="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"

/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK, Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 121 a 173 c 132 g 118 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 gtcgcgcagctgattcc 20
|||||
Db 512 gtcgcgcagctgattcc 528

RESULT 3
BE444713 558 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1137_H03_005ZS wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713
VERSION BE444713.1 GI:9444264
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
1 (bases 1 to 558)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsiao,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
TITLE The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
1..558
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
/clone_1lb="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK, Site_1: EcoRI; Site_2: XhoI; Seeds were

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:12:33 ; Search time 4095.84 Seconds
(without alignments)
65.906 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20

Sequence: 1 tacggtcgcgcgcgcgcgc 20

Scoring table: OLIGO_MDC

Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

EST.*
1: em_estbda.*
2: em_esthum.*
3: em_estlin.*
4: em_estnu.*
5: em_estov.*
6: em_estcpl.*
7: em_estro.*
8: em_estlc.*
9: gb_estl.*
10: gb_est2.*
11: gb_hlc.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_lin.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	17	85.0	422	10	BE443802 WHE1122.B
2	17	85.0	544	10	BE445100 WHE1132.H
3	17	85.0	558	10	BE444713 WHE1137.H
4	17	85.0	610	9	BE195103 HVSMEH008
5	17	85.0	658	10	BE442518 WHE1101.H
6	16	80.0	828	10	BG299722 HVSME002
7	16	80.0	130	10	BM397871 5009-0-38
8	16	80.0	132	10	BM396091 5009-0-17
9	16	80.0	134	10	BM398255 5009-0-42
10	16	80.0	606	10	BI981973 fUS3108.Y
11	16	80.0	640	10	BI888442 ZF637-2-0
12	16	80.0	708	10	BE585978 Est#7PT7
13	15	75.0	237	10	BE423869 WHE0067.F
14	15	75.0	376	9	AI945868 bs17907.Y
15	15	75.0	379	9	AI944952 bs07C12.Y
16	15	75.0	556	12	BH229591 1006153C0
17	15	75.0	568	10	BI628597 RH57079.5

Result	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
1	BE443802	WHE1122.B06.C122S wheat etiolated seedling root normalized CDNA library	BE443802	LOCUS	BE443802.1	GI:9443341	EST.	Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C., and Zhang, D.	The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library	Unpublished (2000)	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818	Location/Qualifiers 1..422 /organism="Triticum aestivum" /cultivar="Chinese Spring" /db_xref="taxon:4565" /clone="WHE1122.B06.C12" /clone_lib="Wheat etiolated seedling root normalized CDNA library" /tissue_type="Root"

ALIGNMENTS

Result	LOCUS	DEFINITION	ACCESSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
1	BE443802	WHE1122.B06.C122S wheat etiolated seedling root normalized CDNA library	BE443802	LOCUS	BE443802.1	GI:9443341	EST.	Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T., Rausch, C.J., Seaton, C.L., Tong, J.C., and Zhang, D.	The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library	Unpublished (2000)	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818	Location/Qualifiers 1..422 /organism="Triticum aestivum" /cultivar="Chinese Spring" /db_xref="taxon:4565" /clone="WHE1122.B06.C12" /clone_lib="Wheat etiolated seedling root normalized CDNA library" /tissue_type="Root"

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Thu Aug 8 09:35:14 2002

us-09-786-105-3.oli.rng

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XX
XX WO9533074-A1.
XX
XX 07-DEC-1995.
XX
XX 26-MAY-1995: 95MO-US06790.
XX
XX 26-MAY-1994: 94US-0250030.
XX
XX (HOFF ) HOFFMANN LA ROCHE INC.
XX (MAYO-) MAYO FOUNDATION.
XX
XX Felmlee TA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
XX Young KK;
XX
XX WPI: 1996-030581/03.
XX
XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX with a primer set that targets portions of the gene encoding rpoB.
XX
XX Disclosure: Fig.3; 54pp: English.
XX
XX This oligonucleotide DNA primer is specific for Mycobacterium
XX tuberculosis, and may be used to amplify a sample DNA by targeting
XX a portion of the gene encoding rpoB. The 1st several bases comprise a
XX nonhybridizing tail consisting of filler bases followed by
XX a restriction site incorporated to facilitate cloning using the
XX amplicon at a later date, if desired. The remaining bases hybridize
XX to bacterial rpoB DNA. The method provides for the detection of M.
XX tuberculosis and the concurrent determination of its drug
XX susceptibility, particularly to rifampin. The method can provide
XX often greater than 95% sensitivity and 100% specificity. The
XX biological sample is a fluid or tissue sample from a human.
XX
XX Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 17; Length 970;
XX Best Local Similarity 100.0%; Pred. No. 0.023;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX 1 tacggtcgcgcgcgcgcgcgc 20
XX |||||||||||||||||||
XX Db 261 tacggtcgcgcgcgcgcgcgc 280
XX
XX RESULT 15
XX AAH51976
XX ID AAH51976 standard; DNA; 3519 BP.
XX
XX AAH51976;
XX
XX 04-SEP-2001 (first entry)
XX
XX Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
XX
XX WO200135317-A1.
XX
XX 17-MAY-2001.
XX
XX 13-NOV-2000; 2000WO-US31152.
XX

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PR 12-NOV-1999: 99US-0165086.
PR 12-NOV-1999: 99US-0165124.
PR 01-FEB-2000: 2000US-0179531.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
XX
XX WPI: 2001-329193/34.
XX P-PSDB: AAG81125.
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
XX involves providing algorithm that analyzes a functional relationship
XX between nucleotide or polypeptide sequences, and comparing the
XX sequences
XX
XX Disclosure: Page 68-69; 207pp: English.
XX
XX This invention relates to a method for identifying a nucleotide or
XX polypeptide sequence that may be a drug target, or essential for growth
XX or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
XX represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
XX tuberculosis proteins which are potential drug targets. The DNA and
XX protein sequences are used to illustrate the method of the invention. The
XX method involves providing an unknown nucleotide or polypeptide sequences,
XX and comparing it to a number of sequences along with at least one
XX algorithm capable of analysing a functional relationship between
XX nucleotide and polypeptide sequences. The method is useful for
XX characterising the function of nucleic acids and polypeptides that may be
XX useful as a target for a drug or essential for the growth or viability of
XX an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
XX
XX Query Match 100.0%; Score 20; DB 22; Length 3519;
XX Best Local Similarity 100.0%; Pred. No. 0.021;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 tacggtcgcgcgcgcgcgcgc 20
XX |||||||||||||||||||
XX Db 1119 tacggtcgcgcgcgcgcgcgc 1138
XX

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Search completed: August 8, 2002, 00:01:25
 Job time: 7614 sec

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Db      18 tacgtcgcgcagctgatcc 37
|||||
RESULT 13
AAA49863
ID      AAA49863 standard; DNA: 480 BP.
XX
AC      AAA49863;
XX
DT      25-SEP-2000 (first entry)
XX
DE      Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KW      Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS      Mycobacterium tuberculosis.
XX
FH      Key
FT      primer_bind      Location/Qualifiers
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FT      primer_bind      372..391
FT                        /*tag= b
FT                        /note= "primer of AAA49824"
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PN      WO200036142-A1.
XX
PD      22-JUN-2000.
XX
PF      10-DEC-1999; 99WO-CA01177.
XX
PR      11-DEC-1998; 98US-0111794.
XX
PA      (VISI-) VISIBLE GENETICS INC.
XX
PI      Shipman R;
XX
DR      WPI; 2000-431611/37.
XX
PT      Method for the detection and characterization of Mycobacterium
PT      tuberculosis with antibiotic resistance in a sample -
XX
PS      Disclosure: Page 5; 43pp; English.
XX
XX      The present sequence is that of the Mycobacterium tuberculosis
XX      rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
XX      cycle sequencing primers (see AAA49823-62) are used for the detection
XX      and analysis of antibiotic resistance-associated mutations in
XX      defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
XX      (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
XX      (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
XX      (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
XX      These primers can be used in a method for the detection and
XX      characterization of M. tuberculosis present in a sputum sample.
XX      The method involves performing a sequencing procedure, with or
XX      without prior amplification, to detect the presence of M.
XX      tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
XX      and 23S genes for the presence of antibiotic-inducing mutations.
XX      If M. tuberculosis is detected, a second sequencing procedure is
XX      performed on the sample to evaluate additional genes for the
XX      presence of antibiotic resistance-inducing mutations. Genotypic
XX      tests are rapid, sensitive and accurate providing information as to
XX      antibiotic treatment options.
XX
SQ      Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;
Query Match      100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Db      41 tacgtcgcgcagctgatcc 60
|||||
RESULT 14
AAT09676
ID      AAT09676 standard; DNA: 970 BP.
XX
AC      AAT09676;
XX
DT      15-OCT-1996 (first entry)
XX
DE      Mycobacterium tuberculosis rpoB gene DNA sequence.
XX
KW      Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
XX      polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS      Mycobacterium tuberculosis.
XX
FH      Key
FT      primer_bind      Location/Qualifiers
FT                        10..27
FT                        /*tag= a
FT                        /note= "primer FENLFF"
FT      primer_bind      226..243
FT                        /*tag= b
FT                        /note= "primer DDIDHL"
FT      primer_bind      226..240
FT                        /*tag= c
FT                        /note= "primer DDIDH"
FT      primer_bind      338..364
FT                        /*tag= d
FT                        /note= "primer rpo95"
FT      primer_bind      348..373
FT                        /*tag= e
FT                        /note= "primer rpo105"
FT      primer_bind      354..373
FT                        /*tag= f
FT                        /note= "primer KY290"
FT      primer_bind      372..373
FT                        /*tag= g
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      433..434
FT                        /*tag= h
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      438
FT                        /*tag= i
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      468..469
FT                        /*tag= j
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      486
FT                        /*tag= k
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      501
FT                        /*tag= l
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      516
FT                        /*tag= m
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      516..535
FT                        /*tag= n
FT                        /note= "primer rpo273"
FT      primer_bind      525
FT                        /*tag= o
FT                        /note= "M. tuberculosis signature nucleotide"
FT      primer_bind      525..541
FT                        /*tag= p
FT                        /note= "primer KY292"
FT      primer_bind      536..562
FT                        /*tag= q
FT      primer_bind      /note= "primer rpo293"
FT      primer_bind      640..666
FT                        /*tag= r
```


DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
XX probe -
XX
XX Disclosure; Page 21; 74pp; English.
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgacc 20
|||||
DB 5 tacggtcgcgcgagctgacc 24

RESULT 9
AAS99527
ID AAS99527 standard; DNA; 306 BP.
XX
AC AAS99527;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #2.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium africanum.
OS
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
XX probe -
PS Disclosure; Page 21; 74pp; English.

XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of
CC mycobacterial rpoB gene and the detection probe is comprised of one or
CC more modified codons of mycobacterial rpoB gene. The method involves
CC amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction
CC (PCR) and discriminating species by fluorescent intensity corresponding
CC to a particular species. The specimen is preferably uncultured sputum,
CC blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569
CC represent mycobacterium species identification probes and primers of the
CC invention.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match 100.0%; Score 20; DB 24; Length 306;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcgagctgacc 20
|||||
DB 5 tacggtcgcgcgagctgacc 24

RESULT 10
AAS99530
ID AAS99530 standard; DNA; 306 BP.
XX
AC AAS99530;
XX
DT 12-MAR-2002 (first entry)
XX
DE Mycobacterium species identification primer #5.
XX
KW Drug resistance detection; mycobacterial species identification; probe;
KW oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
OS Mycobacterium bovis.
OS
PN WO200192573-A1.
XX
PD 06-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-KR00904.
XX
PR 30-MAY-2000; 2000KR-0029369.
XX
PA (BIOM-) BIOMEDLAB CO LTD.
XX
PI Kim H, Kim N, Yoon S, Kim J, Park M;
XX
DR WPI; 2002-075472/10.
XX
XX kit for mycobacterial species identification and drug resistance
PT detection, has oligonucleotide chip with species identification probe,
PT a mycobacterial drug-resistance detection probe, and its contrast group
XX probe -
PS Disclosure; Page 21; 74pp; English.
XX
XX The invention relates to a diagnostic kit for mycobacterial species
CC identification and drug resistance detection comprising an
CC oligonucleotide chip including a species identification probe, a
CC mycobacterial drug-resistance detection probe, a contrast group probe
CC corresponding to each drug resistance detection probe, and a marker for
CC detecting a hybridisation of the oligonucleotide chip and a specimen. The
CC identification probe is comprised of species-specific DNA sequences of


```
ID AAX27179 standard; DNA: 306 BP.
XX
XX AAX27179;
AC
XX 27-MAY-1999 (first entry)
DT
XX
XX RpoB gene fragment.
DE
XX
XX RpoB gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
KW
XX
XX Mycobacteria bovis.
OS
XX
XX MO9905316-A1.
PN
XX 04-FEB-1999.
PD
XX
XX 28-JUL-1998; 98KR-0000228.
PF
XX
XX 28-JUL-1997; 97KR-0035501.
PR
XX
XX (BION-) BIONEER CORP.
PA
XX
XX Kim B, Kook Y;
PI
XX
XX WPI; 1998-539367/46.
DR
XX
XX New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PS species, useful for detecting and identifying mycobacterial species
XX
XX Claim 8; Page 64; 91pp; English.
XX
XX This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX Sequence 306 BP; 56 A; 96 C; 107 G; 47 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 19; Length 306;
XX Best Local Similarity 100.0%; Pred. No. 0.025;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tacggtcggcgagctgaccc 20
XX ||||||||||||||||
XX Db 5 tacggtcggcgagctgaccc 24
XX
XX
XX RESULT 7
XX AAX27180
XX ID AAX27180 standard; DNA: 306 BP.
XX
XX AAX27180;
AC
XX
XX 27-MAY-1999 (first entry)
DT
XX
XX RpoB gene fragment.
DE
XX
XX RpoB gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
KW
XX
XX Mycobacteria bovis.
OS
XX
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PN MO9905316-A1.
XX
XX 04-FEB-1999.
PD
XX
XX 28-JUL-1998; 98KR-0000228.
PF
XX
XX 28-JUL-1997; 97KR-0035501.
PR
XX
XX (BION-) BIONEER CORP.
PA
XX
XX Kim B, Kook Y;
PI
XX
XX WPI; 1998-539367/46.
DR
XX
XX New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the rpoB gene from mycobacterial
PS species, useful for detecting and identifying mycobacterial species
XX
XX Claim 9; Page 64; 91pp; English.
XX
XX This sequence represents a mycobacterial rpoB gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the rpoB gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the rpoB gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in M. tuberculosis.
XX
XX Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
SQ
XX
XX Query Match 100.0%; Score 20; DB 19; Length 306;
XX Best Local Similarity 100.0%; Pred. No. 0.025;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 tacggtcggcgagctgaccc 20
XX ||||||||||||||||
XX Db 5 tacggtcggcgagctgaccc 24
XX
XX
XX RESULT 8
XX AAS99526
XX ID AAS99526 standard; DNA: 306 BP.
XX
XX AAS99526;
AC
XX
XX 12-MAR-2002 (first entry)
DT
XX
XX Mycobacterium species identification primer #1.
DE
XX
XX Drug resistance detection; mycobacterial species identification; probe;
KM oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
KW primer.
XX
XX Mycobacterium tuberculosis.
OS
XX
XX WO200192573-A1.
PN
XX
XX 06-DEC-2001.
PD
XX
XX 30-MAY-2001; 2001WO-KR00904.
PF
XX
XX 30-MAY-2000; 2000KR-0029369.
PR
XX
XX (BION-) BIOMEDLAB CO LTD.
PA
XX
XX Kim H, Kim N, Yoon S, Kim J, Park M;
PI
XX
```

CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpoB*, *kacB*, *rpsL*/*sl2*
CC and *23S* genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 20; DB 21; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgattcc 20
|||||
Db 1 tacgctcgagcagctgattcc 20

RESULT 4
AAx27214
ID AAx27214 standard; DNA; 306 BP.
XX
AC AAx27214;
XX
DT 27-MAY-1999 (first entry)
XX
DE *rpoB* gene fragment.
XX
KW *rpoB* gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
OS *Mycobacteria tuberculosis*.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *rpoB* gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 43; Page 75-76; 91pp; English.

This sequence represents a mycobacterial *rpoB* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpoB* gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the *rpoB* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 306;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgattcc 20
|||||
Db 5 tacgctcgagcagctgattcc 24

RESULT 5
AAx27175
ID AAx27175 standard; DNA; 306 BP.
XX
AC AAx27175;
XX
DT 27-MAY-1999 (first entry)
XX
DE *rpoB* gene fragment.
XX
KW *rpoB* gene; mycobacteria; phylogenetic tree construction;
KM mycobacterial species identification; phylogenetic analysis; ss.
XX
OS *Mycobacteria africanum*.
XX
PN WO9905316-A1.
XX
PD 04-FEB-1999.
XX
PF 28-JUL-1998; 98KR-0000228.
XX
PR 28-JUL-1997; 97KR-0035501.
XX
PA (BION-) BIONEER CORP.
XX
PI Kim B, Kook Y;
XX
DR WPI; 1998-539367/46.
XX
PT New pair of polymerase chain reaction (PCR) primers - for
PT sequence-specific amplification of the *rpoB* gene from mycobacterial
PT species, useful for detecting and identifying mycobacterial species
XX
PS Claim 4; Page 62-63; 91pp; English.

This sequence represents a mycobacterial *rpoB* gene fragment, that is
CC amplified using the PCR primers of the invention. The primers form a
CC method of detecting and identifying mycobacterial species by constructing
CC a phylogenetic tree for the species. The use of the primers for
CC sequence-specific amplification of the *rpoB* gene (encoding the beta
CC subunit of RNA polymerase) from mycobacterial species provides an
CC efficient way of characterising these species. In addition to
CC phylogenetic analysis, the *rpoB* gene can be used as an alternative to
CC the 16S rRNA gene because it has four subunits, which are highly
CC conserved throughout prokaryotes. The method is particularly useful for
CC slow growing, fastidious or uncultivable mycobacteria. Also, rifampin
CC susceptibility can be simultaneously determined in *M. tuberculosis*.
XX
SQ Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 20; DB 19; Length 306;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacgctcgagcagctgattcc 20
|||||
Db 5 tacgctcgagcagctgattcc 24

RESULT 6
AAx27179

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
PS Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. lepre
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgattcc 20
Db 1 tacggtcgcgcagctgattcc 20
|||||

RESULT 2
AAA49823
ID AAA49823 standard; DNA; 20 BP.
XX
AC AAA49823:
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 4; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgattcc 20
Db 1 tacggtcgcgcagctgattcc 20
|||||

RESULT 3
AAA49825
ID AAA49825 standard; DNA; 20 BP.
XX
AC AAA49825:
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.
XX
KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;
KW ss.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200036142-A1.
XX
PD 22-JUN-2000.
XX
PF 10-DEC-1999; 99WO-CA01177.
XX
PR 11-DEC-1998; 98US-0111794.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Shipman R;
XX
DR WPI: 2000-431611/37.
XX
PT Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Claim 4; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826
CC and with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

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OM nucleic - nucleic search, using sw model

Run on: August 8, 2002, 00:01:22 : Search time 562.71 seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20
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Scoring table: OLIGO_NUC
Gapop 60.0, Gapext 60.0

Searched: 1736436 segs, 858457221 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	20	100.0	306	19	AA27215
6	20	100.0	306	19	AA27179
7	20	100.0	306	19	AA27180
8	20	100.0	306	24	AA59526
9	20	100.0	306	24	AA59527

10	20	100.0	306	24	AA59530	Mycobacterium spec
11	20	100.0	306	24	AA59531	Mycobacterium spec
12	20	100.0	432	14	AAQ61457	M.tuberculosis rpo
13	20	100.0	480	21	AAA49863	Mycobacterium tube
14	20	100.0	970	17	AA709676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AA474651	Mycobacterium tube
18	20	100.0	3853	21	AA489994	M. tuberculosis rp
19	19	95.0	306	19	AA27217	Mycobacterium spec
20	19	95.0	306	24	AA59551	Propionibacterium
21	19	95.0	21500	23	AA59633	M. tuberculosis rp
22	18	90.0	25	17	AA12091	Mycobacterium tube
23	18	90.0	87	22	AA288922	Mycobacterium tube
24	16	80.0	306	19	AA27212	RpoB gene fragment
25	16	80.0	306	19	AA27218	RpoB gene fragment
26	16	80.0	306	19	AA27193	RpoB gene fragment
27	16	80.0	306	19	AA27196	RpoB gene fragment
28	16	80.0	306	19	AA27204	RpoB gene fragment
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30	16	80.0	306	19	AA27182	RpoB gene fragment
31	16	80.0	306	19	AA27183	RpoB gene fragment
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34	16	80.0	306	24	AA59557	Mycobacterium spec
35	16	80.0	306	24	AA59560	Mycobacterium spec
36	16	80.0	306	24	AA59565	Mycobacterium spec
37	16	80.0	306	24	AA59568	Mycobacterium spec
38	16	80.0	27426	23	AA59541	Propionibacterium
39	15	75.0	1092	22	AA502316	B. subtilis DNA en
40	15	75.0	2488	23	AB144021	Pseudomonas aerugi
41	15	75.0	2772	23	AA54170	Drosophila melanog
42	15	75.0	4544	23	AB144020	Mycobacterium tube
43	15	75.0	4403765	22	AA19683	Mycobacterium tube
44	15	75.0	4411529	22	AA19682	Expression vector
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ALIGNMENTS

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AC AA12092:
XX
DT 10-JUL-1996 (first entry)
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DE M. tuberculosis rpoB gene fragment amplification primer p2.
XX
XX Antibiotic resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifampicin; species identification; ss.
XX
OS Synthetic.
XX
PN W09533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EF02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
( INNO- ) INNOGENETICS NV.
XX De Beenhouwer H, Jannes G, Machtelinckx L, Portels F;
XX Rossau R;
XX WPI: 1996-040250/04.
XX
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Thu Aug 8 09:35:14 2002

us-09-786-105-3.oli.rge

ORGANISM
Mycobacterium tuberculosis
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 3534)
Bergerson, M.G., Bolsajnot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J. and Roy, P.H.
TITLE
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
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/strain="Rv"
/db_xref="taxon:1773"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.
VERSION U12205
KEYWORDS U12205.1 GI:515684
SOURCE
ORGANISM
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkert, T.
TITLE
The rpoB gene of Mycobacterium tuberculosis
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 3853)
Imboden, P.
TITLE
Direct Submision
JOURNAL
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
FEATURES
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MSMERVVRERMTQDVEATTPQTLINIRVVAATKEFEQTSLSQFMQNNELSLT
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FGIETPYRKVVDGVSDGIVYLTADDEEDHVAQANSPLDAGRFEVPRVLRKAP
EVEYVPSSEVDVDSPPROMSVATAMIPLEHDDNRALMGANMORAVPLVREAP
LVCTGHELRALIDATSSSGESEIVEVSADYTYVHNDGTRRTYMRKFRASNGTC
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TIKS"
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Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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variation	191	/phenotype="rifampicin resistant"
variation	194	/phenotype="rifampicin resistant in association with mutation 203 T"
variation	203	/replace="c"
variation	208..210	/phenotype="rifampicin resistant"
variation	232	/replace="g"
variation	233	/phenotype="rifampicin resistant"
variation	233	/replace="a"
variation	233	/phenotype="rifampicin resistant"
variation	234	/replace="g"
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variation	248	/replace="g"
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DEFINITION	Sequence 59 from patent US 5851763.	432 bp	DNA	linear	PAT 29-SEP-1999
ACCESSION	AR067448				
VERSION	AR067448.1	GI:5998670			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 432)				
	Heym,B., Cole,S., Young,D., Zhang,Y., Honore,N., Telenti,A. and				
	Boomer,T.				
	Rapid detection of antibiotic resistance in mycobacterium				
	tuberculosis				
	Patent: US 5851763-A 59 22-DEC-1998;				
JOURNAL	location/qualifiers				
FEATURES	1..432				
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ORIGIN					

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Best Local Similarity	100.0%	Pred. NC	4.3				
Matches	20	Conservative	0	Mismatches	0	Indels	0
						Gaps	0

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Db      18  TACGGTCGGCGAGCTGATCC 37

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RESULT 13

LOCUS	I50706	970 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 1 from patent US 5643723.				
ACCESSION	I50706				
VERSION	I50706.1	GI:2472409			

SOURCE

Unclassified.
1 (bases 1 to 970)
REFERENCE
AUTHORS
Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T.A., Roberts, G.D.

TITLE	JOURNAL	FEATURES
Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens	Patent: US 5643723-A 1 01-JUL-1997;	Location/Qualifiers

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RESULT 14
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LOCUS	AX111339	3534 bp	DNA	linear	PAT 30-APR-2001
DEFINITION	Sequence	2072	from Patent WO0123604.		

VERSION	AX111339.1	GI:13927631
KEYWORDS		
SOURCE	Mycobacterium tuberculosis.	

Mycobacterium tuberculosis.

Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 7
LOCUS ARI57007 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION ARI57007
VERSION ARI57007.1 GI:15125711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y.-H. and Kim,B.-J.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
source 1..306
Location/Qualifiers
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

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DEFINITION Sequence 7 from patent US 6242584.
ACCESSION ARI57008
VERSION ARI57008.1 GI:15125712
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
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Location/Qualifiers
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

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LOCUS ARI57042 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION ARI57042
VERSION ARI57042.1 GI:15125746
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
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Location/Qualifiers
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

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LOCUS ARI57051 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION ARI57051
VERSION ARI57051.1 GI:15125755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 306)
Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of ipob gene
JOURNAL Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
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Location/Qualifiers
BASE COUNT 56 a 94 c 108 g 48 t
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 TACGGTCGGCGAGCTGATCC 24

RESULT 11
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
Mycobacterium tuberculosis (strain H37) DNA.
Mycobacterium tuberculosis
ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriinae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
1 (bases 1 to 432)
Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,J., Walter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

	Db	5	TACGGTCGGGAGCTGATCC	24	
RESULT	4				
LOCUS	AF057453			306 bp	DNA linear BCT 17-SEP-1998
DEFINITION	Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.				
ACCESSION	AF057453				
VERSION	AF057453.1				
KEYWORDS	GI:5902493				
SOURCE					
ORGANISM	Mycobacterium bovis BCG. Mycobacterium bovis BCG Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 306) Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H. Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)				
REFERENCE	J. Clin. Microbiol. 37 (6), 1714-1720 (1999)				
AUTHORS	99262756 10325313				
TITLE	2 (bases 1 to 306) Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y. Direct Submission Submitted (06-Apr-1998) Microbiology, Seoul National University College of Medicine, 28 Yongsun-dong, Chongno-gu, Seoul 110-799, Korea				
FEATURES					
source	Location/Qualifiers 1..306 /organism="Mycobacterium bovis BCG" /strain="Tokyo 1172" /db_xref="taxon:33892" <1..>306 /gene="rpoB" /locus_tag="rpoB" /transl_table=1 /codon_start=3 /product="RNA polymerase beta" /protein_id="A055517.1" /db_xref="GI:5902494" /translation="RTVGEILQNIIRVSGMSRMERVREMTTDDVEAITPOTLINRP VVAIKKEFGISQLSDPMDDNNPLSGTLHRRRLSALPGSLSRAGLFEVDVPSH"				
CDS					
gene					
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ORIGIN	95 c				
	108 g				
	47 t				
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Best Local Similarity	100.0%; Prid. No. 4.6;				
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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LOCUS	AF057454			306 bp	DNA linear BCT 08-OCT-1999
DEFINITION	Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.				
ACCESSION	AF057454				
VERSION	AF057454.1				
KEYWORDS	GI:5902495				
SOURCE					
ORGANISM	Mycobacterium tuberculosis. Mycobacterium tuberculosis Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.				

[illegible]

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OM nucleic - nucleic search, using sw model

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Title: US-09-786-105-3

Perfect score: 20
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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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33: em_hlg_inv:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
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1	20	100.0	306	1	AF057450	AF057450 Mycobacte
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7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGRIFRNAP	L05910 Mycobacteri
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	I50706	I50706 Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	U12205 Mycobacteri
16	20	100.0	5084	1	MSGROPH	L27989 Mycobacteri
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTG1376	Z95972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
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21	18	90.0	25	6	AA7816	AA7816 Sequence 30
22	18	90.0	87	6	AX050338	AX050338 Sequence
23	17	85.0	17407	1	AE006976	AE006976 Mycobacte
24	17	85.0	68848	1	MTV043	AL022004 Mycobacte
25	16	80.0	306	1	AF057456	AF057456 Mycobacte
26	16	80.0	306	1	AF057459	AF057459 Mycobacte
27	16	80.0	306	1	AF057460	AF057460 Mycobacte
28	16	80.0	306	1	AF057463	AF057463 Mycobacte
29	16	80.0	306	1	AF057471	AF057471 Mycobacte
30	16	80.0	306	1	AF057473	AF057473 Mycobacte
31	16	80.0	306	1	AF057480	AF057480 Mycobacte
32	16	80.0	306	1	AF057489	AF057489 Mycobacte
33	16	80.0	306	1	AF057496	AF057496 Corynebac
34	16	80.0	306	1	AF173087	AF173087 Mycobacte
35	16	80.0	306	6	AR157005	AR157005 Sequence
36	16	80.0	306	6	AR157010	AR157010 Sequence
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39	16	80.0	306	6	AR157021	AR157021 Sequence
40	16	80.0	306	6	AR157024	AR157024 Sequence
41	16	80.0	306	6	AR157032	AR157032 Sequence
42	16	80.0	306	6	AR157040	AR157040 Sequence
43	16	80.0	306	6	AR157046	AR157046 Sequence
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ALIGNMENTS

RESULT 1	AF057450	306 bp	DNA	linear	BCT 17-SEP-1999
LOCUS	AF057450				
DEFINITION	Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.				
ACCESSION	AF057450				
VERSION	AF057450.1	GI:5902487			
KEYWORDS	Mycobacterium africanum.				
SOURCE	Mycobacterium africanum.				
ORGANISM	Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.				
REFERENCE	1 (bases 1 to 306)				
AUTHORS	Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.				
TITLE	Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)				
JOURNAL	J. Clin. Microbiol. 37 (6), 1714-1720 (1999)				
MEDLINE	99262756				
PUBMED	10325313				
REFERENCE	2 (bases 1 to 306)				
AUTHORS	Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,				

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/protein_id="AAK44924.1"
/db_xref="GI:13880221"
/translation="MIGSHVSPDPPLAAAEAGADVQIFIGNQSKAKPKPRDAA
AKAKTLPITYAPYLINLASANNRRLPSRKILQETCAAADICAAYIVHGAVAD
DNDIDGFORMRKALDRLETEVYVLENGAGDHAMARFPIARLMVIGDTGIFC
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LVAAVKAAGAPVICTADQGRKDDIAFLERTGS"
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ANGGCGRPARPEGVDIGFVRAVADIANNSIDPARVYTGMSNGAIMSTTLACN
STFRAIGVSGTQLDPCOSPRPVYIHIGHADPLVRYHGGPAGFARIDGPVPDLN
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AHFR"
11859. .13487
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putative"
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/db_xref="GI:13880223"
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GAISASCOQRMGELADNRNPILHTHDAYGYRDEVDPAYHELMRTAITHGMHAAP
WADRPGAHVRAKTSYVTEPGHICPISMTYAVPALRYNSLAVYEPILTSTREY
DPELKPATTKAGITAGMSMETEGKSGSDRAGTQATPRADSGYSLTGKKTTSAPMCD
ITVIAQAPDGLSCFLPRVYPDGTRNRNPLQRLDKLGNHANSSEVEYDGAVALWV
GEBRGVPTIIEYNALTRLDCAIGSATSMRTGLTRAHHQAHRKAFGAYLIDQILMRN
VLADIAVEAEATIVAMRMAGATDNVANGNETEALLRRIIGLAARAYWCKRSTAAAE
ALECIGNGYVEDSGMRLYREAPLMGIMESGNVSALDILRAMATRPACVEVEDEL
ARSAGODPRLDGHVERLPDLGDLDTIGYRARKIAEDICLAGSLVRRHGPAAVAA
FLATRLGGOMGAGTWPAGLDLAPILERALVKG"
13498. .14436
/gene="MT0702"
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/note="similar to GP:3885480; identified by sequence
similarity; putative"
/codon_start=1
/transl_table=1
/product="enoyl-CoA hydratase/isomerase family protein"
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/db_xref="GI:13880224"
/translation="MTHAIRPVDFDNLKMTYEVTGRIARTFNRPEKGNATIDTPL
ELSLIVERADLDGVHVLVSGRGEFCAGFDLSAYAESSSTGGGAGYGTIDGKT
OAVNHLPNOPMDPKIDYQMSRFYRGPASLMHADKPTVVKIHGICVAGGTDIALHADQ
VIAAADAKIGTPTRVWGVPFAGLMAHRLSDQRAKRLFTGDCITGQAQAAEWGLAVEA
PEPADLERTERLVARIALPVLNOLIMVKLALNSALLQGVATSRMVSIVFDGAARHT
PEGHAFVADAVEHGFDAVRRDEPFEGDYGRQASRV"
14439. .15161
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/note="identified by Glimmer2; putative"
/codon_start=1
/transl_table=1
/product="hypothetical protein"

Query Match 100.0%; Score 20; DB 1; Length 19352;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcgttcgatgaacc 20
|||||
Db 1709 TACGGCGTTTCATGAACCC 1690

Search completed: August 7, 2002, 23:49:03
Job time: 9217 sec

CC compared to the cleavage products of reference gene sequences. The
 CC method is used for detecting mutation in the human p53 gene; for
 CC identifying strains of microorganisms, especially bacteria selected
 CC from the group of members of the genera Campylobacter,
 CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
 CC The method may also be used for the identification of viruses,
 CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
 CC (SIV). Two primers (AAT9122, AAT9123) were used to amplify a 620 bp
 CC region of the Mycobacterium tuberculosis rpoB gene, which, when
 CC amplified is associated with rifampin resistance. The 620 bp region
 CC amplified spans both the H451Y and S456L mutations. The amplified
 CC fragments are given in AAT9124 (wild type) and AAT9125-26
 CC (mutant sequences).

CC Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgacc 20
 ||||||||||||||||
 Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 8

AAT09676/C
 ID AAT09676 standard; DNA; 970 BP.

AC AAT09676;

DT 15-OCT-1996 (first entry)

XX Mycobacterium tuberculosis rpoB gene DNA sequence.

XX Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;

KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.

XX Mycobacterium tuberculosis.

XX Key Location/Qualifiers

FH primer_bind

FT 10..27 /tag= a

FT /note= "primer FENLFP"

FT primer_bind

FT 226..243 /tag= b

FT /note= "primer DDIDL"

FT primer_bind

FT 226..240 /tag= c

FT /note= "primer DDIDL"

FT primer_bind

FT 338..364 /tag= d

FT /note= "primer rpo95"

FT primer_bind

FT 348..373 /tag= e

FT /note= "primer rpo105"

FT primer_bind

FT 354..373 /tag= f

FT /note= "primer KY290"

FT misc-feature

FT 372..373 /tag= g

FT /note= "M. tuberculosis signature nucleotide"

FT misc-feature

FT 433..434 /tag= h

FT /note= "M. tuberculosis signature nucleotide"

FT misc-feature

FT 438 /tag= i

FT /note= "M. tuberculosis signature nucleotide"

FT misc-feature

FT 468..469 /tag= j

FT /note= "M. tuberculosis signature nucleotide"

FT misc-feature

FT 486 /note= "M. tuberculosis signature nucleotide"

FT /tag= k

FT /note= "M. tuberculosis signature nucleotide"

FT misc-feature

FT 501 /tag= l

FT /note= "M. tuberculosis signature nucleotide"

FT misc-feature

FT 516 /tag= m

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind

FT 516..535 /tag= n

FT /note= "primer rpo273"

FT misc-feature

FT 525 /tag= o

FT /note= "M. tuberculosis signature nucleotide"

FT primer_bind

FT 525..541 /tag= p

FT /note= "primer KY292"

FT primer_bind

FT 536..562 /tag= q

FT /note= "primer rpo293"

FT primer_bind

FT 640..666 /tag= r

FT /note= "primer rpo397"

FT primer_bind

FT 952..966 /tag= s

FT /note= "primer NMORO-1"

FT primer_bind

FT 952..966 /tag= t

FT /note= "primer NMORO-2"

FT

FT

FT

FT

FT

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FT

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FT

FT

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FT

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Query Match 100.0%; Score 20; DB 17; Length 970;

Best Local Similarity 100.0%; Pred. No. 0.0071;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacggcgttcgatgacc 20
 ||||||||||||||||
 Db 671 TACGGCGTTTCGATGAACCC 652

Disclosure: Fig.3; 54pp; English.
 Detection of Mycobacterium tuberculosis - by amplifying sample DNA
 with a primer set that targets portions of the gene encoding rpoB.

This oligonucleotide DNA primer is specific for Mycobacterium
 tuberculosis, and may be used to amplify a sample DNA by targeting
 a portion of the gene encoding rpoB. The 1st several bases comprise a
 nonhybridizing tail consisting of filler bases followed by
 a restriction site incorporated to facilitate cloning using the
 amplicon at a later date, if desired. The remaining bases hybridize
 to bacterial rpoB DNA. The method provides for the detection of M.
 tuberculosis and the concurrent determination of its drug
 susceptibility, particularly to rifampin. The method can provide
 often greater than 95% sensitivity and 100% specificity. The
 biological sample is a fluid or tissue sample from a human.

Sequence 970 BP; 182 A; 302 C; 330 G; 156 T; 0 other;

RESULT	9
AAH51976/c	
ID	AAH51976 standard; DNA; 3519 BP.
XX	
AC	AAH51976;
XX	
D7	04-SEP-2001 (first entry)
XX	
DE	Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX	
KW	Drug target; growth; organism viability; characterisation; ds.
XX	
OS	Mycobacterium tuberculosis.
XX	
PN	WO200135317-A1.
PD	
FD	17-MAY-2001.
XX	
PF	13-NOV-2000; 2000WO-US31152.
XX	
PR	12-NOV-1999; 99US-0165086.
PR	12-NOV-1999; 99US-0165124.
PR	01-FEB-2000; 2000US-0179531.
XX	
PA	(REGC) UNIV CALIFORNIA.
XX	
P1	Eisenberg D, Rotstein SH, Marcotte EM;
XX	
DR	WPI: 2001-329193/34.
DR	P-PSDB; AAG81125.
XX	
PT	Identifying nucleotide or polypeptide sequence for use as drug target,
PT	involves providing algorithm that analyzes a functional relationship
PT	between nucleotide or polypeptide sequences, and comparing the
PT	sequences -
XX	
PS	Disclosure: Page 68-69; 207pp; English.
XX	
CC	This invention relates to a method for identifying a nucleotide or
CC	polypeptide sequence that may be a drug target, or essential for growth
CC	or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC	represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC	tuberculosis proteins which are potential drug targets. The DNA and
CC	protein sequences are used to illustrate the method of the invention. The
CC	method involves providing an unknown nucleotide or polypeptide sequences,
CC	and comparing it to a number of sequences along with at least one
CC	algorithm capable of analysing a functional relationship between
CC	nucleotide and polypeptide sequences. The method is useful for
CC	characterising the function of nucleic acids and polypeptides that may be
CC	useful as a target for a drug or essential for the growth or viability of
CC	an organism.
XX	
SQ	Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
Query Match	100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity	100.0%; Pred. No. 0.0064;
Matches 20; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
OY	1 tacgagcttcgatgaacc 20
Db	1529 TAGGCGTTTCGATGAACCC 1510
RESULT 10	
AAH02079/c	
ID	AAH02079 standard; DNA; 3534 BP.
XX	
AC	AAH02079;
XX	
JT	24-JUL-2001 (first entry)

```

DE  Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
XX  Species specific; genus specific; family specific; probe; detection;
XX  Identification; algal; archaeal; bacterial; fungal; parasitical;
XX  microorganism; diagnosis; translation elongation factor Tu; toxin;
XX  translation elongation factor G; RecA recombinase; resistance;
XX  catalytic subunit of proton-translocating ATPase; antimicrobial;
XX  vaccine; primer; ds.
XX
XX  Mycobacterium tuberculosis.
OS
XX  WO200123604-A2.
XX
XX  05-APR-2001.
XX
XX  28-SEP-2000; 2000WO-COA01150.
XX
XX  28-SEP-1999; 99CA-2283458.
XX  19-MAY-2000; 2000CA-2307010.
XX
XX  (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
XX  Bergeron MG, Boissinot M, Hulersky A, Menard C, Ouellette M;
XX  Picard FJ, Roy PH;
XX  WPI: 2001-245006/25.
XX
XX  Nucleic acid sequences are used to generate universal probes and
XX  primers which can be used to identify and detect the presence of algal,
XX  archaeal, bacterial, fungal and parasitcal species in a test sample -
XX
XX  Disclosure; Page 1478-1479; 1580pp; English.
XX
XX  The present invention describes a method for generating a repertory of
XX  nucleic acids of tut, fus, atpd and/or recA genes from which probes
XX  and/or primers are derived. The method comprises amplifying the nucleic
XX  acids of determined algal, archaeal, bacterial, fungal and parasitcal
XX  species with a combination of defined primer pairs. The method can be
XX  used for producing probes and/or primers for detecting one or more
XX  related microorganisms e.g. algae, archaea, bacteria, fungi and
XX  parasites, for universal detection and for specific and ubiquitous
XX  detection and identification of an algal, archaeal, bacterial, fungal
XX  and parasitcal species, genus, family and group. A nucleic acid (I)
XX  obtained using the method of the invention can be used for the universal
XX  detection of any bacterium, fungus or parasite in a sample and for the
XX  detection of at least one antimicrobial agent resistance gene or at
XX  least one toxin gene. hexa nucleic acids are used for the specific and
XX  ubiquitous detection and for identification of Streptococcus pneumoniae.
XX  (I) can be used to design a therapeutic agent which is effective against
XX  microorganisms. Microbial species or genus or family or phylum or group
XX  which can be detected include Abiotrophia adiacens, Bordetella sp.,
XX  Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
XX  Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
XX  Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
XX  provides faster results than substrate specificity tests as results can
XX  be determined in an hour and improved accuracy is also achieved.
XX  AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX  which are given in the exemplification of the present invention.
XX
XX  Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
XX
XX  Query Match 100.0%; Score 20; DB 22; Length 3534;
XX  Best Local Similarity 100.0%; P-adj. 0.0064;
XX  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX  1 tacggcgttcgatcaacc 20
XX  ||||||||||||||||
XX  Db 1547 TACGGCGTTTCGATCAACC 1528

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AAA74651/C
ID AAA74651 standard; DNA: 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
KW rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PI particularly for detecting rifampin resistance in Mycobacterium
XX tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgattcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||
RESULT 12
ID AAA89994 standard; DNA: 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX

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PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PR 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PI Mycobacterium, comprising detecting mutations in a gene and relating
XX them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such as rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

```

```

Query Match 100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgattcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||
RESULT 13
ID AAT12096 standard; DNA: 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic; resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machelinckx L, Portael F;

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PI Rosau R;
XX WPI: 1996-040250/04.
XX
XX Probes and primers for determ. of antibiotic resistance spectrum of
PI Mycobacterium, opt. coupled with species identification - from
PI different patterns of hybridisation with rpoB gene
XX
XX Claim 22; Page 39; 69pp; English.
XX
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp., from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;

Query Match      95.0%; Score 19; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 19
   |||||||
Db 1 tacggcgttcgatgaacc 19

RESULT 14
AAT09670
ID AAT09670 standard; DNA; 27 BP.
XX
AC AAT09670;
XX
XX 15-OCT-1996 (first entry)
XX
DE Mycobacterium tuberculosis 27-mer oligonucleotide DNA primer rpo397.
XX
KM Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; PCR;
KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.
XX
OS Synthetic.
XX
PN W09533074-A1.
XX
PD 07-DEC-1995.
XX
PF 26-MAY-1995; 95WO-US06790.
XX
PR 26-MAY-1994; 94US-0250030.
XX
PA (HOFF ) HOFFMANN LA ROCHE INC.
PA (MAYO-) MAYO FOUNDATION.
XX
PI Feinlee JA, Hunt JM, Persing DH, Roberts GD, Whelen AC;
PI Young KK;
XX
XX WPI: 1996-030581/03.
XX
XX
XX Detection of Mycobacterium tuberculosis - by amplifying sample DNA
XX with a primer set that targets portions of the gene encoding rpoB.
XX
XX Claim 9; Page 39; 54pp; English.
XX
XX This oligonucleotide DNA primer is specific for Mycobacterium
XX tuberculosis, and may be used to amplify a sample DNA by targeting
XX a portion of the gene encoding rpoB. The method provides for the

```

```

CC detection of M. tuberculosis and the concurrent determination of its
CC drug susceptibility, particularly to rifampicin. The method can
CC provide often greater than 95% sensitivity and 100% specificity.
CC The biological sample is a fluid or tissue sample from a human.
XX
SQ Sequence 27 BP; 6 A; 7 C; 8 G; 6 T; 0 other;

Query Match      75.0%; Score 15; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaacc 20
   |||||||
Db 1 cgttcgatgaacc 15

RESULT 15
AA051532/C
ID AA051532 standard; DNA; 3447 BP.
XX
AC AA051532;
XX
XX 17-MAY-1994 (first entry)
XX
DE M.leprae rpoB gene.
XX
KM rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
KM mutant; ss.
XX
XX Mycobacterium leprae.
XX
XX
XX Key Location/Qualifiers
XX CDS 1..3447
XX FT /*tag= a
XX FT /note= "rifampicin-sensitive; in resistant
XX FT strains the Ser codon (TGC at
XX FT nucleotides 1273-1275) is often mutated
XX FT to a Phe, Met or esp. Leu codon"
XX
XX W09322454-A.
XX
XX 11-NOV-1993.
XX
XX 30-APR-1993; 93WO-EP01063.
XX
XX 17-SEP-1992; 92FR-0011098.
XX
XX 30-APR-1992; 92US-0875940.
XX
XX 14-AUG-1992; 92US-0929206.
XX
XX 16-APR-1993; 93FR-0004545.
XX
XX (ASST-) ASSISTANCE PUBLIQUE.
XX
XX (INSP ) INST PASTEUR.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX
XX (UYBE-) UNIV BERNE.
XX
XX (UYPA-) UNIV CURIE PARIS VI P & M.
XX
PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
PI Young D, Zhang Y;
XX
XX WPI: 1993-368812/46.
XX
XX P-PSDB; AAR43671.
XX
XX
XX Rapid detection of antibiotic resistance in Mycobacteria - esp.
XX isoniazid, rifampicin or streptomycin resistance in tuberculosis
XX by detecting mutation in katG, rpoB or rpsL genes
XX
XX Example 2; Fig 12; 97pp; English.
XX
XX PCR amplification was used to obtain rpoB genes from rifampicin-
XX resistant Mycobacterium leprae strains. A comparison with the
XX sequence of the rpoB gene from sensitive strains (AA051532) revealed
XX mutations in the region encoding amino acids 400-450. A common

```

CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match 70.0%; Score 14; DB 14; Length 3447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 gttcgaatgaacc 20
|||||
DB 1448 GTTCGATGAACCC 1435

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Job time: 7615 sec

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-786-105-4

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Post-processing: listing first 45 summaries

Database:

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4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	85.0	234	10	W06754
2	17	85.0	579	10	W06754 SMEST0390 S
3	16	80.0	624	10	T24127
4	15	75.0	624	10	BE896357
5	15	75.0	884	10	BM077908
6	15	75.0	452	9	AM694629
7	15	75.0	517	12	TA247H04P
8	15	75.0	536	12	A0783856
9	15	75.0	537	12	TA140G03P
10	15	75.0	540	12	TA190A10P
11	15	75.0	631	12	BH615799
12	15	75.0	690	9	BE053145
13	15	75.0	1033	12	CNS040XP
14	15	75.0	1218	10	BM007170
15	14	70.0	247	9	AV640031
16	14	70.0	269	9	AV640876
17	14	70.0	288	9	BH177553
	14	70.0	336	12	A0605040

C	18	14	70.0	390	9	AV644609	AV644609
C	19	14	70.0	416	9	AJ284239	AJ284239
C	20	14	70.0	421	12	A2813806	A2813806
C	21	14	70.0	428	10	BK252718	BK252718
C	22	14	70.0	431	9	AM280184	AM280184
C	23	14	70.0	466	9	AF051116	AF051116
C	24	14	70.0	472	10	BE449520	BE449520
C	25	14	70.0	474	9	AV396989	AV396989
C	26	14	70.0	476	9	A1483656	A1483656
C	27	14	70.0	477	9	A1488127	A1488127
C	28	14	70.0	489	9	AM618736	AM618736
C	29	14	70.0	497	9	AV643117	AV643117
C	30	14	70.0	508	9	AV642711	AV642711
C	31	14	70.0	518	9	AV642141	AV642141
C	32	14	70.0	525	9	AM650840	AM650840
C	33	14	70.0	531	9	AV642766	AV642766
C	34	14	70.0	544	12	A0843909	A0843909
C	35	14	70.0	556	9	AM155814	AM155814
C	36	14	70.0	562	12	BH487728	BH487728
C	37	14	70.0	566	9	AV631818	AV631818
C	38	14	70.0	582	12	CNS01K68	CNS01K68
C	39	14	70.0	626	9	AM442770	AM442770
C	40	14	70.0	626	9	BB640393	BB640393
C	41	14	70.0	628	10	BF270176	BF270176
C	42	14	70.0	664	10	BG102752	BG102752
C	43	14	70.0	670	12	A0943645	A0943645
C	44	14	70.0	672	12	A0943372	A0943372
C	45	14	70.0	676	9	A1491107	A1491107

ALIGNMENTS

RESULT 1
W06754/c 234 bp mRNA linear EST 01-JUL-1996
LOCUS SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
ACCESSION W06754
VERSION W06754.1 GI:1444974
KEYWORDS EST.
SOURCE Schistosoma mansoni.
ORGANISM Schistosoma mansoni.
REFERENCE Strigellidida, Schistosomatidae: Trematoda: Digenea:
Eukaryota: Metazoa: Platyhelminthes: Schistosoma.
AUTHORS Franco, G.R. and Pena, S.D.J.
TITLE Unpublished
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Bioquimica
Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.
Location/Qualifiers
1..234
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBE73"
/clone_lib="Schistosoma mansoni, adult worm, Gloria
Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector, Site_1: NotI, Site_2: HindIII;
Total cellular RNA from male and female adult worms was
extracted according to a modification (Puissant, C. and
Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
Guandine Thiocyanate procedure (Chomczynski, P. and

Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+ RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a two fold molar excess of a NotI/HindIII digested plasmid DNA (Jaefmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells."

BASE COUNT 49 a 84 c 66 g 33 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaa 17
|||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 2

T24127/c 579 bp mRNA linear EST 27-FEB-1995
LOCUS SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA SMPBC65 3', mRNA sequence.
T24127
T24127.1 GI:529730

EST.
Schistosoma mansoni.
SOURCE

REFERENCE Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
AUTHORS Strigelidida; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 579)
Franco,G.R., Adams,M.D., Soares,M.B., Sampson,A.J.G., Venter,J.C.
and Pena,S.D.J.

TITLE Identification of new Schistosoma mansoni genes by the EST strategy
JOURNAL using a directional cDNA library
MEDLINE Gene 152, 141-147 (1995)
COMMENT 95137379
Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genetica-Bioquimica, Departamento de Biologia
Imunologia
Instituto de Ciencias Biologicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward

FEATURES
SOURCE Location/Qualifiers

1..579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone_lib="Schistosoma mansoni, adult worm, Gloria
Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
Total cellular RNA from male and female adult worms was
extracted according to a modification (Puissant, C. and
Houdeline, L. M. Biofeedback 8, 148-149, 1990) of the
Guandinine Thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by oligo dT column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid
DNA (Jaefmid BA vector, a phagemid derived from pEMBL,
Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and
electroporated into E. coli strain DH10B (BRL). The
library was amplified and further selected for clones
containing long inserts (>500 bp) by purification of the
plasmid DNA from a fragment of a 1% low-melting-point
agarose gel, containing the smear of the library and
electroporation into DH10B cells."

BASE COUNT 102 a 206 c 179 g 88 t 4 others
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaa 17
|||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 3

BE896357 624 bp mRNA linear EST 20-OCT-2000
LOCUS 601439015F1 NIH_MGC_72 Homo sapiens cDNA IMAGE:3924266 5',
DEFINITION mRNA sequence.
T24127
T24127.1 GI:10360678

EST.
BE896357
BE896357.1 GI:10360678
EST.
SOURCE

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 624)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DC/DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers

FEATURES
SOURCE 1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 155 a 209 c 150 g 110 t
ORIGIN

Query Match 80.0%; Score 16; DB 10; Length 624;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ggcgttcgatgacc 20
|||||
Db 582 GCGTTTCGATGACC 597

RESULT 4
 BM077908 384 bp mRNA linear EST 14-NOV-2001
 LOCUS p21i06.y1 Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy Chlapelli
 DEFINITION McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
 ACCESSION BM077908
 VERSION BM077908.1 GI:16924944
 KEYWORDS EST, hookworm.
 SOURCE Ancylostoma caninum
 ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
 REFERENCE 1 (bases 1 to 384)
 AUTHORS McCarter,J., Clifton,S., Chlapelli,B., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C., Underwood,K., Steptoe,M., Allen,M., Pearson,B., Swaller,T., Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE The Washington Univ. Nematode EST Project, 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 The library was constructed by Claire Murphy, Brandt Chlapelli, and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center.
 FEATURES
 source
 1..384
 /organism="Ancylostoma caninum"
 /db_xref="taxon:29170"
 /clone_lib="Ancylostoma caninum L3 SS SL1 TOPO v1 Murphy Chlapelli McCarter"
 /dev_stage="Serum stimulated L3"
 /lab_host="DH10B"
 /note="Vector: PCRIT-TOPO (Invitrogen); Site1: EcoRI, Site2: EcoRI; The library was constructed by Claire Murphy, Brandt Chlapelli, and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Ancylostoma caninum SS/L3 cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCRIT-TOPO(Invitrogen) following the TOPO TA cloning protocol. Nematodes were provided by Dr. Prema Arasu (Prema.Arasu@ncsu.edu) of North Carolina State University in Raleigh, NC."

BASE COUNT 116 a 71 c 85 g 112 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 10; Length 384;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 4 ggcgttcgagtaac 18
 ||||||||||||||||
 Db 324 GGCCTTCGATGAAAC 338
 RESULT 5
 AM694629 452 bp mRNA linear EST 21-DEC-2000
 LOCUS NF078E03ST 5', mRNA sequence.
 DEFINITION
 ACCESSION AM694629
 VERSION AM694629.2 GI:11957636

KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales; Medicago.
 REFERENCE 1 (bases 1 to 452)
 AUTHORS He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
 TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 JOURNAL Medicago truncatula stem library
 COMMENT Unpublished (2000)
 On Apr 14, 2000 this sequence version replaced gi:7569391.
 CONTACT: Dixon RA
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7302
 Fax: 580 221 7380
 Email: radixon@noble.org
 Insert Length: 736 Std Error: 0.00
 Plate: 078 row: E column: 03
 Seq primer: TCACACGGAACACGCTATGAC.
 FEATURES
 source
 1..452
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone_lib="NF078E03ST"
 /dev_stage="developing stem"
 /issue_type="stem"
 /note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
 BASE COUNT 152 a 94 c 91 g 115 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 9; Length 452;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 cgttcgagtaacc 20
 ||||||||||||||||
 Db 338 CGTTTCGATGAACC 324
 RESULT 6
 TA247H04P 517 bp DNA linear GSS 13-DEC-2000
 LOCUS T. brucei sheared genomic DNA clone 247h04, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL483262
 VERSION AL483262.1 GI:11848938
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei.
 ORGANISM Trypanosoma brucei
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 REFERENCE 1 (bases 1 to 517)
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajendram,M.A. and Barrell,B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA. E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.

FEATURES
source
1. 517
Location/Qualifiers

/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="247h04"

BASE COUNT 116 a 116 c 135 g 150 t
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 517;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgac 18
|||||
Db 293 ggcgttcgatgac 307

RESULT 7
AQ783856 536 bp DNA linear GSS 03-AUG-1999
LOCUS
DEFINITION HS.2001.A2.F09.T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=18 Row=K, DNA sequence.
ACCESSION AQ783856
VERSION AQ783856.1 GI:5691480
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 536)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: <http://www.htsc.washington.edu>
Plate: 2001 row: K column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 536.
Location/Qualifiers

1. 536
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=2001 Col=18 Row=K"
/clone.lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm. Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

BASE COUNT 160 a 124 c 92 g 156 t 4 others
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 536;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 cgttcgatgaccc 20
|||||
Db 506 cgttcgatgaccc 520

RESULT 8
TA140G03P 537 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 140g03, forward sequence, genomic survey sequence.
ACCESSION AL466454
VERSION AL466454.1 GI:11835809
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma
1 (bases 1 to 537)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

REFERENCE 1 (bases 1 to 537)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

COMMENT

Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
1. 537
Location/Qualifiers
/organism="Trypanosoma brucei"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="140g03"

FEATURES
source

BASE COUNT 108 a 120 c 110 g 199 t
ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 537;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgac 18
|||||
Db 85 ggcgttcgatgac 99

RESULT 9
TA190A10P/c 540 bp DNA linear GSS 13-DEC-2000
LOCUS
DEFINITION T. brucei sheared genomic DNA clone 190a10, forward sequence, genomic survey sequence.
ACCESSION AL477985
VERSION AL477985.1 GI:11841795
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma

REFERENCE 1 (bases 1 to 540)
 AUTHORS Hall, N., Bowman, S., Leonard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrell, B.G.
 TITLE Direct Submission
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nhle@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/projects/T_brucei/.
 FEATURES
 source Location/Qualifiers
 1..540
 /organism="Trypanosoma brucei"
 /strain="TREU927"
 /db_xref="taxon:5691"
 /clone="190a10"
 BASE COUNT 177 a 118 c 126 g 119 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 12; Length 540;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ggcgttcgatgaac 18
 |||||
 DB 325 GCGCTTCGATGAC 311
 RESULT 10
 LOCUS BH615799 631 bp DNA linear GSS 28-JAN-2002
 DEFINITION BMBAC304F01SP6 PSU Brugia malayi Genomic Bac Library 3 Brugia
 malayi genomic, DNA sequence.
 ACCESSION BH615799
 VERSION BH615799.1 GI:18380487
 KEYWORDS GSS.
 SOURCE Brugia malayi.
 ORGANISM Brugia malayi.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Splturida; Filarioidea;
 Onchocercidae; Brugia.
 1 (bases 1 to 631)
 Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
 J., Guilleno, D., Slatko, B. and Blaxter, M.
 Genome survey sequences from the human parasitic nematode Brugia
 malayi
 JOURNAL Unpublished (2000)
 COMMENT Contact: Blaxter ML
 Institute of Cell, Animal and Population Biology
 University of Edinburgh
 Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
 3JF, UK
 Tel: +44 131 650 6760
 Fax: +44 131 670 5450
 Email: mark.blaxter@sanger.ac.uk
 Sequenced from the Brugia malayi BAC library constructed by Claire
 Whitton and Dr Mike Quail. The sequence was generated by The
 Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
 collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
 Edinburgh, UK.
 Seq primer: SP6 (ATTAGCTGACACTATAG)
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..631
 /organism="Brugia malayi"
 /strain="TBS"
 /db_xref="taxon:6279"
 /clone_lib="Brugia malayi Genomic Bac Library 3"
 /sex="Mixed (male and female)"
 /tissue_type="whole parasite"
 /dev_stage="microfilaria (L1)"
 /note="Vector: pBACE3.6; Site_1: BamH I; Brugia malayi
 genomic DNA was partially cleaved with Sau3A I and size
 fractionated. 7,392 clones were generated with mean insert
 size ~48 kbp. The library was constructed by Claire
 Whitton, Blaxter Nematode Genetics Lab, University of
 Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
 Unit, The Sanger Centre, Cambridge, UK."
 BASE COUNT 196 a 94 c 142 g 199 t
 ORIGIN
 Query Match 75.0%; Score 15; DB 12; Length 631;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 acggcgttcgatga 16
 |||||
 DB 606 ACCGCGTTGCGATGA 620
 RESULT 11
 LOCUS BE053145 690 bp mRNA linear EST 07-MAR-2001
 DEFINITION GA_Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
 arboreum cDNA clone GA_Ea0002K16f, mRNA sequence.
 ACCESSION BE053145
 VERSION BE053145.2 GI:13244065
 KEYWORDS EST.
 SOURCE Gossypium arboreum.
 ORGANISM Gossypium arboreum.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
 1 (bases 1 to 690)
 Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry
 D., Wood, T.C., Leslie, A. and Wilkins, T.A.
 An integrated analysis of the genetics, development, and evolution
 of the cotton fiber
 JOURNAL Unpublished (2000)
 COMMENT On Jun 8, 2000 this sequence version replaced gi:8380201.
 Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: twing@clemson.edu
 Seq primer: TAATAGACTGACTATAGGG
 High quality sequence stop: 550.
 FEATURES
 source Location/Qualifiers
 1..690
 /organism="Gossypium arboreum"
 /strain="AKA"
 /cultivar="8400"
 /db_xref="taxon:29729"
 /clone_lib="GA_Ea0002K16f"
 /tissue_type="Fibers isolated from bolls harvested 7-10
 dpa"
 /lab_host="E. coli"
 /note="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"
 BASE COUNT 169 a 132 c 151 g 236 t
 ORIGIN

Query Match 75.0%; Score 15; DB 9; Length 690;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggcgttcgatgaac 18
|||||
Db 567 GGCCTTCGATGAC 581

RESULT 12
CNS040Y/C 1033 bp DNA linear GSS 18-MAY-2000
LOCUS Tetradon nigroviridis genome survey sequence T7 end of clone
DEFINITION 073004 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL269530.1 GI:7991421
VERSION AL269530
KEYWORDS GSS: genome survey sequence.
SOURCE Tetradon nigroviridis.
ORGANISM Tetradon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetradon.
REFERENCE 1 (bases 1 to 1033)
AUTHORS Roest-Crollius,H., Jallou,O., Dasilva,C., Filames,C., Fisher,C.,
Bonneau,L., Billault,A., Quetler,F., Saurin,W., Bernot,A. and
Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1033)
AUTHORS Roest-Crollius,H., Jallou,O., Dasilva,C., Bonneau,L., Fisher,C.,
Bernot,A., Filames,C., Wincker,P., Brotlier,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using
Tetradon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1033)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
FEATURES
source
1..1033
/organism="Tetradon nigroviridis"
/db_xref="taxon:99883"
/clone="073004"
/clone_1lb="G"
/note="Genoscope sequence ID : COBG073BH02LP1-end : T7"

BASE COUNT 270 a 222 c 276 g 261 t 4 others

ORIGIN

Query Match 75.0%; Score 15; DB 12; Length 1033;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 cggcgttcgatgaac 17
|||||
Db 460 CGGCTTCGATGAC 446

RESULT 13
BM007170 1218 bp mRNA linear EST 30-OCT-2001
LOCUS 603614933N1 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:5420816 3',
DEFINITION mRNA sequence.
ACCESSION BM007170

VERSION BM007170.1 GI:16521524
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1218)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: gcraps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LCM1876 row: a column: 09
High quality sequence start: 25
High quality sequence stop: 313.
Location/Qualifiers
1..1218
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5420816"
/clone_1lb="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: pancreas; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC library." 4 others

BASE COUNT 370 a 446 c 244 g 154 t

ORIGIN

Query Match 75.0%; Score 15; DB 10; Length 1218;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 cgttcgatgaaccc 20
|||||
Db 364 CGTTCGATGACCC 378

RESULT 14
AV640031/c 247 bp mRNA linear EST 15-DEC-2000
LOCUS AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii
DEFINITION CDNA clone HCL009D04_r 5', mRNA sequence.
ACCESSION AV640031
VERSION AV640031.1 GI:10783359
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
REFERENCE 1 (bases 1 to 247)
AUTHORS Asamizu,E., Miura,K., Kuchio,K., Inoue,Y., Fukuzawa,H., Ohyama,K.,
Nakamura,Y. and Tabata,S.
TITLE Generation of expressed sequence tags from low-CO2 and high-CO2
adapted cells of Chlamydomonas reinhardtii
JOURNAL DNA Res. 7 (5), 305-307 (2000)
MEDLINE 20539644
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute

Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.
 Location/Qualifiers

FEATURES
 SOURCE

1. 247
 /organism="Chlamydomonas reinhardtii"
 /strain="C9"
 /db_xref="taxon:3055"
 /clone="HCL009b04_r"
 /clone_1lb="Chlamydomonas reinhardtii 5% CO₂"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; The cDNA library was constructed from cells cultured
 in a medium with bubbling air containing 5% carbon
 dioxide"

BASE COUNT 61 a 79 c 54 g 53 t
 ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 247;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
 |||||
 DB 245 GGCGTTTCGATGAA 232

RESULT 15
 AV640876/c

LOCUS AV640876 269 bp mRNA linear EST 15-DEC-2000
 DEFINITION AV640876 Chlamydomonas reinhardtii 5% CO₂ Chlamydomonas reinhardtii
 CDNA clone HCL024a01_r 5', mRNA sequence.

ACCESSION AV640876
 VERSION AV640876.1 GI:10784204
 KEYWORDS EST.
 SOURCE Chlamydomonas reinhardtii.
 ORGANISM Chlamydomonas reinhardtii.
 Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 Chlamydomonadaceae; Chlamydomonas.

REFERENCE 1 (bases 1 to 269)
 Asamizu, E., Miura, K., Kuchio, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,
 Nakamura, Y. and Tabata, S.
 Generation of expressed sequence tags from low-CO₂ and high-CO₂
 adapted cells of Chlamydomonas reinhardtii

JOURNAL DNA Res. 7 (5), 305-307 (2000)
 MEDLINE 20539644
 COMMENT

Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.
 Location/Qualifiers

FEATURES
 SOURCE

1. 269
 /organism="Chlamydomonas reinhardtii"
 /strain="C9"
 /db_xref="taxon:3055"
 /clone="HCL024a01_r"
 /clone_1lb="Chlamydomonas reinhardtii 5% CO₂"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI; The cDNA library was constructed from cells cultured
 in a medium with bubbling air containing 5% carbon
 dioxide"

BASE COUNT 65 a 85 c 60 g 59 t
 ORIGIN

Query Match 70.0%; Score 14; DB 9; Length 269;
 Best Local Similarity 100.0%; Pred. No. 1.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggcgttcgatgaa 17
 |||||
 DB 254 GGCGTTTCGATGAA 241

Search completed: August 7, 2002, 23:12:33
 Job time: 11072 sec

Thu Aug 8 09:35:18 2002

us-09-786-105-4.oli.rst

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:21 ; Search time 146.61 Seconds
(Without alignments)
33,508 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 tacgagcttcgaggaacc 20

Scoring table: IDENTITY_NUC

Searched: Gapp 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA :
1: /cgn2_6/prodata/2/lna/5A.COMB.seq : *
2: /cgn2_6/prodata/2/lna/5B.COMB.seq : *
3: /cgn2_6/prodata/2/lna/6A.COMB.seq : *
4: /cgn2_6/prodata/2/lna/6B.COMB.seq : *
5: /cgn2_6/prodata/2/lna/PCTUS.COMB.seq : *
6: /cgn2_6/prodata/2/lna/backfiles1.seq : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	20	100.0	432	2	US-08-313-185-59	Sequence 59, Appl
C 2	20	100.0	432	3	US-09-082-614A-59	Sequence 59, Appl
C 3	20	100.0	620	2	US-08-757-653-135	Sequence 135, App
C 4	20	100.0	620	2	US-08-757-653-136	Sequence 136, App
C 5	20	100.0	620	2	US-08-757-653-137	Sequence 137, App
C 6	20	100.0	620	2	US-08-757-653-138	Sequence 138, App
C 7	20	100.0	620	2	US-08-757-653-139	Sequence 139, App
C 8	20	100.0	620	2	US-08-757-653-140	Sequence 140, App
C 9	20	100.0	706	4	US-08-797-812-24	Sequence 24, Appl
C 10	20	100.0	970	5	PCT-US95-06790-1	Sequence 1, Appl
C 11	20	100.0	970	5	US-08-250-030-1	Sequence 1, Appl
C 12	19	95.0	19	4	US-08-750-088A-71	Sequence 71, Appl
C 13	18.4	92.0	3447	2	US-08-313-185-57	Sequence 57, Appl
C 14	18.4	92.0	3447	3	US-09-082-614A-57	Sequence 57, Appl
C 15	15.8	79.0	1472	1	US-08-622-354-2	Sequence 2, Appl
C 16	15.8	79.0	2310	1	US-08-622-354-1	Sequence 1, Appl
C 17	15.2	76.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 18	15	75.0	27	1	US-08-250-030-9	Sequence 9, Appl
C 19	15	75.0	27	5	PCT-US95-06790-9	Sequence 9, Appl
C 20	14.2	71.0	1081	4	US-09-372-422A-33	Sequence 33, Appl
C 21	14.2	71.0	1153	4	US-09-372-448A-5	Sequence 5, Appl
C 22	14.2	71.0	2262	3	US-08-674-887A-5	Sequence 5, Appl
C 23	14.2	71.0	2262	3	US-08-951-844-5	Sequence 5, Appl
C 24	13.8	69.0	117	5	US-08-299-498A-59	Sequence 59, Appl
C 25	13.8	69.0	117	5	PCT-US95-10813-59	Sequence 59, Appl
C 26	13.8	69.0	776	4	US-09-372-422A-43	Sequence 43, Appl
C 27	13.8	69.0	1100	4	US-09-372-422A-47	Sequence 47, Appl

C 28	13.8	69.0	1176	3	US-08-911-853-34	Sequence 34, Appl
C 29	13.8	69.0	1176	4	US-09-479-409-34	Sequence 34, Appl
C 30	13.8	69.0	1176	4	US-09-479-453-34	Sequence 34, Appl
C 31	13.8	69.0	1375	4	US-09-372-422A-37	Sequence 37, Appl
C 32	13.8	69.0	1485	4	US-09-372-422A-39	Sequence 39, Appl
C 33	13.8	69.0	2394	3	US-09-027-064-1	Sequence 1, Appl
C 34	13.8	69.0	2394	4	US-09-271-815-1	Sequence 1, Appl
C 35	13.8	69.0	17612	3	US-08-911-853-29	Sequence 29, Appl
C 36	13.8	69.0	17612	4	US-09-479-409-29	Sequence 29, Appl
C 37	13.8	69.0	17612	4	US-09-479-453-29	Sequence 29, Appl
C 38	13.8	69.0	4403765	4	US-09-103-840A-2	Sequence 2, Appl
C 39	13.6	68.0	585	4	US-09-404-671-3	Sequence 3, Appl
C 40	13.6	68.0	686	4	US-09-372-422A-45	Sequence 45, Appl
C 41	13.6	68.0	699	4	US-08-998-416-705	Sequence 705, Appl
C 42	13.6	68.0	999	4	US-09-177-234-7	Sequence 7, Appl
C 43	13.6	68.0	1087	4	US-09-372-422A-29	Sequence 29, Appl
C 44	13.6	68.0	1209	1	US-08-314-309A-5	Sequence 5, Appl
C 45	13.6	68.0	1513	1	US-08-314-309A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
: Sequence 59, Application US/08313185
: Patent No. 5851763
: GENERAL INFORMATION:
: APPLICANT: Heym, Beate
: APPLICANT: Cole, Stewart
: APPLICANT: Young, Douglas
: APPLICANT: Zhang, Ying
: APPLICANT: Honore, Nadine
: APPLICANT: Telenti, Amalio
: APPLICANT: Bodmer, Thomas
: TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1300 I Street, N.W.
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/313,185
: FILING DATE: 12-OCT-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Meyers, Kenneth J.
: REGISTRATION NUMBER: 25,146
: REFERENCE/DOCKET NUMBER: 02356, 0068-00000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 408-4000
: TELEFAX: (202) 408-4400
: INFORMATION FOR SEQ ID NO: 59:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 432 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
US-09-082-614A-59/C

; Sequence 59, Application US/09082614A

; Patent No. 6124098

; GENERAL INFORMATION:

; APPLICANT: Heym, Beate

; APPLICANT: Cole, Stewart

; APPLICANT: Young, Douglas

; APPLICANT: Zhang, Ying

; APPLICANT: Honore, Nadine

; APPLICANT: Telenit, Amalio

; APPLICANT: Bodmer, Thomas

; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

; TITLE OF INVENTION: In Mycobacterium Tuberculosis

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flanegan, Henderson, Farabow, Garrett &

; ADDRESSEE: Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/082.614A

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/313,185

; FILING DATE: 12-OCT-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0068-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-09-082-614A-59

Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 432;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
US-08-757-653-135/C
; Sequence 135, Application US/08757653
; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/757,653

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ingolia, Diane E.

; REGISTRATION NUMBER: 40,027

; REFERENCE/DOCKET NUMBER: FORS-02565

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 705-8410

; TELEFAX: (415) 397-8338

; INFORMATION FOR SEQ ID NO: 135:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 620 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-757-653-135

Query Match

Best Local Similarity 100.0%; Score 20; DB 2; Length 620;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/C

; Sequence 136, Application US/08757653

; Patent No. 5843669

; GENERAL INFORMATION:

; APPLICANT: Kaiser, Michael W.

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Lyamichev, Natasha

; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

; NUMBER OF SEQUENCES: 190

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Medlen & Carroll, LLP

; STREET: 220 Montgomery Street, Suite 2200

; CITY: San Francisco

; STATE: California

; COUNTRY: United States Of America

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/c
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

```

CORRESPONDENCE ADDRESS:
ADDRESS: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-139

Query Match      100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
    |||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
US-08-757-653-140
Sequence 140, Application US/08/57653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamlichev, Victor I.
APPLICANT: Lyamlichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable Fen-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
```

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 140:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-140

Query Match      100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
    |||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
US-08-797-812-24/C
Sequence 24, Application US/08/797812
Patent No. 6228575
GENERAL INFORMATION:
APPLICANT: Gingeras, Thomas A.
APPLICANT: Mack, David
APPLICANT: Chee, Mark S.
APPLICANT: Bereno, Anthony J.
APPLICANT: Strayer, Lubert
APPLICANT: Ghandour, Ghassan
APPLICANT: Wang, Ching
TITLE OF INVENTION: Chip-Based Species Identification and
TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,812
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,339
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 16528X-018550
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 24:
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SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACCC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M. 33,977
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150,1050S1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150,105M01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,088A
; FILING DATE: 21-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: GOLDSTEIN, JORGE A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 1657,0010000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-750-088A-71

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Query Match          95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 tacggcgcttcgatgaacc 19
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Db 1 TACGGCGCTTCGATGACCC 19

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RESULT 13
US-08-313-185-57/C
; Sequence 57, Application US/08313185
; Patent No. 5851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,185
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356,0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-313-185-57

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```

Query Match          92.0%; Score 18.4; DB 2; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 tacggcgcttcgatgaacc 20
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Db 1454 TACGGCTTCGATGACCC 1435

```

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RESULT 14
US-09-082-614A-57/C
; Sequence 57, Application US/09082614A
; Patent No. 6124098
; GENERAL INFORMATION:
; APPLICANT: Heym, Beate
; APPLICANT: Cole, Stewart
; APPLICANT: Young, Douglas
; APPLICANT: Zhang, Ying
; APPLICANT: Honore, Nadine
; APPLICANT: Telenti, Amalio
; APPLICANT: Bodmer, Thomas
; TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
; TITLE OF INVENTION: In Mycobacterium Tuberculosis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,614A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/313,185
; FILING DATE: 12-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356,0068-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-082-614A-57

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```

Query Match          92.0%; Score 18.4; DB 3; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
    |||||

```

DB 1454 TACGGTGTTCGATGAACCC 1435

RESULT 15

US-08-622-354-2/c
; Sequence 2, Application US/08622354
; Patent No. 5827518
; GENERAL INFORMATION:
; APPLICANT: WEBB, Bruce A.
; APPLICANT: CUI, Liwang
; TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE
; TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: VA
; COUNTRY: US
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/622,354
; FILING DATE: 27-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1472 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 190..1155
; US-08-622-354-2

Query Match 79.0%; Score 15.8; DB 1; Length 1472;
Best Local Similarity 89.5%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 tacggcgttcgataacc 19
||||| ||||| ||||| |||||
DB 1105 TACGGGTTTACATGAACC 1087

Search completed: August 7, 2002, 21:54:25
Job time: 24020 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:21; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 tacggcgttcgtatgaacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estcov:*
6: em_estcpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pin:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	396	10	BF220419 NXCI_146
2	17.4	87.0	399	10	BF169611 NXCI_125
3	17.4	87.0	452	10	BC040291 NXCI_110
4	17.4	87.0	539	9	AA556698 553 Lob10
5	17.4	87.0	545	10	BF777209 NXCI_066
6	17.4	85.0	234	10	W06754 SMEST0390 S
7	17.4	85.0	579	10	T24127 SMEST0325 S
8	16.8	84.0	277	9	AA734164 vs19g12.r
9	16.4	82.0	576	10	BF252921 EST420184
10	16.4	82.0	624	10	BE896357 601439015
11	16.4	82.0	631	12	BH615799 BMBC304F
12	16.4	82.0	961	12	AG141490 Pan trogl
13	15.8	79.0	213	9	AM064407 SP0996 KR
14	15.8	79.0	436	9	AI1496312 s005008.y
15	15.8	79.0	582	12	CNS01K68 Anopheles
16	15.8	79.0	637	10	BC908684 Talr1170D
17	15.8	79.0	650	10	BC908616 Talr1169H

C 18	15.8	79.0	752	12	CNS03678	AL229661 Tetradon
C 19	15.8	79.0	775	12	A2125549	A2125549 OSJNB009
C 20	15.8	79.0	885	12	CNS02B0Q	AL189251 Tetradon
C 21	15.8	79.0	913	10	BF204833	BF204833 60167133
C 22	15.8	79.0	1029	12	CNS0549K	AL320465 Tetradon
C 23	15.8	79.0	1411	10	BI663170	BI663170 603286791
C 24	15.6	78.0	885	12	CNS01K02	AL147715 Anopheles
C 25	15.4	77.0	248	10	BC140300	BC140300 EST480742
C 26	15.4	77.0	269	9	AV640876	AV640876 AV640876
C 27	15.4	77.0	384	10	BM077908	BM077908 pb21906.y
C 28	15.4	77.0	390	9	AV644609	AV644609 AV644609
C 29	15.4	77.0	467	12	CNS03FUV	AL242176 Tetradon
C 30	15.4	77.0	474	9	AV396989	AV396989 AV396989
C 31	15.4	77.0	489	9	AM618736	AM618736 EST320722
C 32	15.4	77.0	497	9	AV643117	AV643117 AV643117
C 33	15.4	77.0	508	9	AV642711	AV642711 AV642711
C 34	15.4	77.0	518	9	AV642141	AV642141 AV642141
C 35	15.4	77.0	531	9	AV642766	AV642766 AV642766
C 36	15.4	77.0	532	10	BI506216	BI506216 BB170018A
C 37	15.4	77.0	536	12	AO783856	AO783856 HS_2001.A
C 38	15.4	77.0	548	12	AQ497017	AQ497017 HS_5197.B
C 39	15.4	77.0	566	9	AV631818	AV631818 AV631818
C 40	15.4	77.0	788	10	BE566696	BE566696 601339653
C 41	15.2	76.0	146	10	BM096759	BM096759 EBMA07.SQ
C 42	15.2	76.0	200	10	BM098906	BM098906 EBP105.SQ
C 43	15.2	76.0	205	12	A2577000	A2577000 06d05.SHO
C 44	15.2	76.0	269	10	BF953380	BF953380 RC3-NM019
C 45	15.2	76.0	317	9	BB501888	BB501888 BB501888

ALIGNMENTS

RESULT 1
LOCUS BF220419 396 bp mRNA linear EST 08-NOV-2000
DEFINITION NXCI_146.A06.F NXCI (Nsif Xylem Compression wood Inclined) Pinus
taeda cDNA clone NXCI_146.A06 5', mRNA sequence.

ACCESSION BF220419.1 GI:11126551

VERSION BF220419.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 396)
Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3

FEATURES

source

Location/Qualifiers
1..396
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXCI_146.A06"
/clone_1lb="NXCI (Nsif Xylem Compression wood Inclined)"
/tissue="Xylem"
/cell_type="Compression"
/dev_stage="juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site:1: Eco RI; Site:2: XhoI
The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of

all three genotypes was used for the library. oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI Bluescript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCAGCAG'."

BASE COUNT 71 a 84 c 122 g 110 t 9 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
||||| |||||||||
Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 2
BF169611 399 bp mRNA linear EST 30-OCT-2000
LOCUS NXCI_125_C05_F NXCI (NsI Xylem Compression wood Inclined) Pinus
DEFINITION taeda cDNA clone NXCI_125_C05 5', mRNA sequence.
ACCESSION BF169611 GI:11054228
VERSION BF169611.1 GI:11054228
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 399)
AUTHORS Sederoff, R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers
1..399
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone_1b="NXCI_125_C05"
/clone_1lb="NXCI (NsI Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of
all three genotypes was used for the library. oligo-dT
primed cDNA was directionally cloned into the EcoRI-XhoI
Bluescript SK vector arms. NOTE: The sequences contain a
'cDNA adapter' between the EcoRI site and the start of the
EST. The adapter sequence is 'AATTCGGCAGCAG'."

BASE COUNT 71 a 84 c 121 g 121 t 2 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 399;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
||||| |||||||||

Db 15 ACGGCGCTTCGATGAACCC 33

RESULT 3
BG040291 452 bp mRNA linear EST 24-JAN-2001
LOCUS NXSI_110_F06_F NXSI (NsI Xylem Side wood Inclined) Pinus taeda cDNA
DEFINITION clone NXSI_110_F06 5', mRNA sequence.
ACCESSION BG040291 GI:12482876
VERSION BG040291.1 GI:12482876
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 452)
AUTHORS Sederoff, R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers
1..452
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone_1b="NXSI_110_F06"
/clone_1lb="NXSI (NsI Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dT primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTCGGCAGCAG'."

BASE COUNT 71 a 122 c 146 g 95 t 18 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 452;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgatgaacc 20
||||| |||||||||
Db 329 ACGGCGCTTCGATGAACCC 347

RESULT 4
AA556698 539 bp mRNA linear EST 28-AUG-1998
LOCUS 553 loblolly pine CA Pinus taeda cDNA clone ICABAG, mRNA sequence.
DEFINITION AA556698
ACCESSION AA556698 GI:3365713
VERSION AA556698.1 GI:3365713
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 539)

AUTHORS Allona, I., Quim, M., Shoop, E., Swope, K., St. Cyr, S., Carlis, J.,
TITLE Retzel, J., Retzel, E., Campbell, M.M., Sederoff, R. and Whetten, R.W.
JOURNAL Analysis of xylem formation in pine by cDNA sequencing
MEDLINE Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
COMMENT 96356220

CONTACT: Ross Whetten
 Forest Biotechnology Group
 North Carolina State University
 Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
 NC, 27695-8008
 Tel: 919-515-7800
 Fax: 919-515-7801
 Email: rosswhet@unity.ncsu.edu
Seq primer: T3.

FEATURES
source location/Qualifiers

1..539
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="1CABAG"
 /clone_lib="loblolly pine CA"
 /tissue_type="xylem"
 /lab_host="SOLR"
 /note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
 The result of subtraction of C library with N library.
 Immature xylem from the underside of inclined stems of
 differentiating compression wood was substracted with
 immature xylem from the side of inclined stems of
 differentiating wood. A mixture of four genotypes were
 used. Oligo-dT primed cDNA was directionally cloned into
 the EcoRI-XhoI lambda-ZAP vector arms"
BASE COUNT 102 a 120 c 156 g 150 t 11 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 539;
Best Local Similarity 94.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 acggcgcttcgatgaacc 20
 ||||| ||||| ||||| |||||
Db 145 ACGGCGCTTCGATGACCC 163

RESULT 5
LOCUS BF777209 545 bp mRNA linear EST 12-JAN-2001
DEFINITION NXS1_066_E05_F NXS1 (Nsf xylem side wood inclined) Pinus taeda cDNA
ACCESSION NXS1_066_E05 5', mRNA sequence.
VERSION BF777209
KEYWORDS BF777209.1 GI:12125109
SOURCE EST.
ORGANISM loblolly pine.
Pinus taeda
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 545)
AUTHORS Sederoff, R.
TITLE Molecular Basis of Wood Formation in the Pine Megagenome
JOURNAL Unpublished (2000)
COMMENT Contact: Johnson, Arthur
 North Carolina State University
 Tel: 919 515 7801
 Fax: 919 515 7800
 Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source location/Qualifiers

1..545
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXSI_066_E05"
 /clone_lib="NXSI (Nsf xylem side wood inclined)"

/tissue_type="xylem"
 /cell_type="side"
 /dev_stage="juvenile"
 /lab_host="XLI-Blue"
 /note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
 ; The library is from early (spring) wood, taken from
 three six-year old trees (three different genotypes), in
 the juvenile phase. These trees were induced to form side
 wood by bending to a 45 degree angle and tying them to the
 ground. Differentiating xylem was harvested from the sides
 of the inclined stems, and a mixture of all three
 genotypes was used for the library. Oligo-dT primed cDNA
 was directionally cloned into the EcoRI-XhoI primed cDNA
 vector arms. NOTE: The sequences contain a 'cDNA adapter'
 between the EcoRI site and the start of the EST. The
 adapter sequence is 'ATTCGCGACGAG'."
BASE COUNT 92 a 142 c 167 g 132 t 12 others
ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 545;
Best Local Similarity 94.7%; Pred. No. 78;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 acggcgcttcgatgaacc 20
 ||||| ||||| ||||| |||||
Db 256 ACGGCGCTTCGATGACCC 274

RESULT 6
LOCUS W06754 234 bp mRNA linear EST 01-JUL-1996
DEFINITION SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco
ACCESSION Schistosoma mansoni cDNA clone SMPBE73 end, mRNA sequence.
VERSION W06754
KEYWORDS W06754.1 GI:1444974
SOURCE EST.
ORGANISM Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.

REFERENCE 1 (bases 1 to 234)
AUTHORS Franco, G.R. and Pena, S.D.J.
JOURNAL Unpublished (1996)
COMMENT Contact: Franco G.R. and Pena S.D.J.
 Laboratorio de Genetica-Bioquimica, Departamento de Biologia
 Inmunologia
 Instituto de Ciencias Biologicas, Universidade Federal de Minas
 Gerais
 Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
 Tel: (5531)4415611
 Fax: (5531)4415409
 Email: gfranco@mono.icb.ufmg.br
Seq primer: M13 Forward.

FEATURES
source location/Qualifiers

1..234
 /organism="Schistosoma mansoni"
 /strain="NMRI"
 /db_xref="taxon:6183"
 /clone="SMPBE73"
 /clone_lib="Schistosoma mansoni, adult worm, Gloria
 Franco"
 /lab_host="DH10B, JM109"
 /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
 Total cellular RNA from male and female adult worms was
 extracted according to a modification (Pulsant, C. and
 Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
 Guanidine Thiocyanate procedure (Chomczynski, P. and
 Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
 RNA was purified by oligo dT column and cDNA was
 synthesized as described previously (Adams, M. D. et al.
 Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid DNA (lambdafmd BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4: 373-389, 1993), and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

Query Match	85.0%	Score 17	DB 10	Length 234
Best Local Similarity	100.0%	Pred. No.	1e+02	
Matches 17	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
Oy      1   tacgacgttcgatga    17  
        |||  
Db      64   TACGGCGTTTCGATGA    48
```

RESULT	7
T24127/c	
LOCUS	579 bp mRNA
DEFINITION	linear EST 27-FEB-1995
ACCESSION	
	T24127
	SMSST0325 Schistosoma mansoni, adult worm, Gloria Franco
	Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
	U01127

SOURCE ORGANISM	Schistosoma mansoni, Schistosoma mansoni
-----------------	---

REFERENCE	AUTHORS
1 (bases 1 to 579)	Franco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C.

TITLE	IDENTIFICATION OF NEW SCHISTOSOMA MANSONI GENES BY THE EST STRATEGY USING A DIRECTIONAL cDNA LIBRARY
JOURNAL	Gene 152, 141-147 (1995)

COMMENT
Contact: Franco G.R. and Pena S.D.J.
Laboratório de Genética-Bioquímica, Departamento de Bioquímica e Imunologia
Instituto de Ciências Biológicas, Universidade Federal de Minas Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@monocb.ufmg.br
Seq primer: M13 Forward.

```

FEATURES
    source
        location/Qualifiers
            1..579
                /organism="Schistosoma mansoni"
                /strain="NMRI"
                /db_xref="taxon:6183"
                /clone="SMPBC65"
                /clone_11b="Schistosoma mansoni, adult worm, Gloria
                Franco"
                /lab_host="DH10B, JM109"
                /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
                Total cellular RNA from male and female adult worms was
                extracted according to a modification (Puissant, C. and
                Houdeline, L. M. Biofeedback 8, 148-159, 1990) of the
                Guanidine thiocyanate procedure (Chomczynski, P. and
                Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
                RNA was purified by oligo dt column and cDNA was
                synthesized as described previously (Adams, M. D. et al.
                Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
                two fold molar excess of a NotI/HindIII digested plasmid
                DNA (1afmid BA vector, a phagemid derived from pEMBL,
                Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and
                electroporated into E. coli strain DH10B (BRL). The

```

BASE COUNT	ORIGIN
102 a	library was amplified and further selected for clones containing long inserts (>500 bp) by ligation of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells.
206 c	"
179 g	"
88 t	"
4	others

Query Match	85.0%;	Score 17;	DB 10;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 1.3e+02;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	tacgcgcttcgatgaa	17
Db	75	TACGGCGCTTCGATGAA	59

RESULT	8
AA734164	
LOCUS	
DEFINITION	277 bp mRNA linear EST 07-JAN-1998
	vs19942.1 Barstead mouse irradiated colon MPRB7 Mus musculus cDNA
	clone IMAGE:1138726 5' similar to gb:X80659 M.musculus L26 mRNA
	(MOUSE);, mRNA sequence.

SOURCE	house mouse.
ORGANISM	Mus musculus

REFERENCE
AUTHORS
1 (bases 1 to 277)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

TITLE	JOURNAL	COMMENT
The Washu-HIMI Mouse EST Project	Unpublished (1996)	Contact: Mairia W/Mouse EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@elwatson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:61998
Trace considered overall poor quality
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.

```

location/Qualifiers
1..277
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="1138726"
/clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoRI; Site_2: NotI. Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gys. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
15TGTTCAGCATCTCACTGGACGCGCCGCCCTTTTTTTTTTTTTTTTTTT
TACT3'; double-stranded cDNA was ligated to Eco RI
adaptors (AATTCGATCTTG), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library constructed by Bob Barstead."
BASE COUNT
64 a 59 c 92 g 62 t
RRIGIN

```


Query Match 84.0%; Score 16.8; DB 9; Length 277;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 taccgcttcgatgaacc 20
||||| ||||||| |||||
Db 47 TACGGCTTCGATGACCC 66

RESULT 9
BF252921/c 576 bp mRNA linear EST 15-NOV-2001
LOCUS EST420184 Coccidioides immitis spherule CDNA library Coccidioides
DEFINITION immitis CDNA clone C18BC49 5' sequence, mRNA sequence.
ACCESSION BF252921 GI:16933064
VERSION BF252921.1 GI:16933064
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Oryzales; mitosporic Oryzales; Coccidioides.
REFERENCE 1 (bases 1 to 576)
AUTHORS Gardner, M.J., and Kirkland, T.
TITLE Generation of ESTs from Coccidioides immitis spherule CDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers
1. 576
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C18BC49"
/clone_1lb="Coccidioides immitis spherule CDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 113 a 186 c 176 g 101 t
ORIGIN

Query Match 82.0%; Score 16.4; DB 10; Length 576;
Best Local Similarity 94.4%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cggcgcttcgatgaacc 20
||||| ||||||| |||||
Db 241 CGGCGTTCGATGACCC 224

RESULT 10
BE896357 624 bp mRNA linear EST 20-OCT-2000
LOCUS 601439015F1 NIH_MGC_72 Homo sapiens CDNA clone IMAGE:3924266 5',
DEFINITION mRNA sequence.
ACCESSION BE896357
VERSION BE896357.1 GI:10360678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCPD/DRP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
plate: LLM8761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers
1. 624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_1lb="NIH_MGC_72"
/issue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 155 a 209 c 150 g 110 t
ORIGIN

Query Match 82.0%; Score 16.4; DB 10; Length 624;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cggcgcttcgatgaacc 20
||||| ||||||| |||||
Db 580 CGGCGTTCGATGACCC 597

RESULT 11
BH615799 631 bp DNA linear GSS 28-JAN-2002
LOCUS BMBAC304F01SP6_P5U Brugia malayi genomic Bac library 3 Brugia
DEFINITION malayi genomic, DNA sequence.
ACCESSION BH615799
VERSION BH615799.1 GI:18380487
KEYWORDS GSS.
SOURCE Brugia malayi.
ORGANISM Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 631)
AUTHORS Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster
, J., Guilliano, D., Slatko, B. and Blaxter, M.
TITLE Genome survey sequences from the human parasitic nematode Brugia
malayi
JOURNAL Unpublished (2000)
COMMENT Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JF, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAAP, University of Edinburgh,
Edinburgh, UK.
Seq primer: SP6 (ATTAGTGCACACTATAG)
Class: BAC ends.
Location/Qualifiers
1. 631
/organism="Brugia malayi"

/strain="TRS"
/db_xref="taxon:6279"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/note="Vector: pBAC3.6; Site 1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size -48 kbp. The library was constructed by Claire Whitton, Blaxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

BASE COUNT 196 a 94 c 142 g 199 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 631;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgcttcgatgaacc 19
|||||
Db 606 ACGCGCTTCGATGATCC 623

RESULT 12
AG141490 961 bp DNA linear GSS 08-JAN-2002
LOCUS AG141490/c
DEFINITION Pan troglodytes DNA, clone: RP43-001J13.TJ, genomic survey
sequence.
ACCESSION AG141490
VERSION AG141490.1 GI:16671168
KEYWORDS GSS: GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RP43-Chimpanzee
Male BAC Library clone:RP43-001J13.TJ.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library RP43-43
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 961)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Toto, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9111, Fax: 81-45-503-9170
URL: http://hsp.gsc.riken.go.jp/
COMMENT Clones are derived from the chimpanzee BAC library RP43-43 This BAC
end was generated during the Rsp process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..961
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J13.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RP43-Chimpanzee Male BAC Library"
BASE COUNT 255 a 299 c 145 g 252 t 10 others
ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 961;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 acggcgcttcgatgaacc 19
|||||
Db 746 ACGCGCTTCGATGATGACC 729

RESULT 13
AM064407 213 bp mRNA linear EST 07-DEC-2000
LOCUS AM064407/c
DEFINITION SP09936 KRIIB Human CD4 Intrathymic T-cell cDNA library Homo sapiens
CDNA 3', mRNA sequence.
ACCESSION AM064407
VERSION AM064407.1 GI:8888344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Goh, S.-H., Park, J.-H., Lee, Y.-S., Lee, H.-G., Yoo, H.-S., Lee, I.-C.,
Park, J.-H., Kim, Y.-S. and Lee, C.-C.
TITLE Gene expression profile and identification of differentially
expressed transcripts during human intrathymic T-cell development
JOURNAL by cDNA sequencing analysis
MEDLINE Genomics 70 (1), 1-18 (2000)
COMMENT 20541704
Contact: Sung-Ho Goh
Genome Center
Korea Research Institute of Bioscience and Biotechnology
Kun-dong 52, Yu Sung-gu, Daejeon 305-353, Republic of Korea
Tel: 82-42-860-4473
Fax: 82-42-860-4479
Email: gohshemail.kribb.re.kr
Seq primer: T7
High quality sequence stop: 213
POLYA-No.

FEATURES
source
1..213
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KRIIB Human CD4 Intrathymic T-cell cDNA
library"
/tissue_type="thymus"
/cell_type="intrathymic T-cell"
/dev_stage="CD3+4+8- single positive stage"
/note="Vector: pGEM-T; cDNA was made from total
cytoplasmic RNA of sorted human intrathymic CD3+4+8-
T-cell, adaptor ligated, amplified with PCR, and cloned
into pGEM-T vector."

BASE COUNT 41 a 59 c 72 g 40 t 1 others
ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 213;
Best Local Similarity 89.5%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 acggcgcttcgatgaacc 20
|||||
Db 43 ACGCGCTTCGATGATGACC 25

RESULT 14
A1496312 436 bp mRNA linear EST 30-NOV-2001
LOCUS sb05b08.y1 Gm-cl004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION Gm-cl004-7888 5' similar to TR:Q92388 Q92388 CNG1 GENE. ;, mRNA
sequence.
ACCESSION A1496312

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:04:01 ; Search time 568.44 Seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 tacggcgttcgataaaccc 20

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*

23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	20	100.0	20	AAA49824
2	20	100.0	21	AAA49826
3	20	100.0	20	AAA49826
4	20	100.0	432	14
5	20	100.0	480	21
6	20	100.0	620	17
7	20	100.0	620	17
8	20	100.0	970	17
9	20	100.0	3519	22

C	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
C	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
C	12	20	100.0	3853	21	AAA89994	M. tuberculosis rp
C	13	19	95.0	19	17	AAI12096	M. tuberculosis rp
C	14	18.4	92.0	3447	14	AAO51352	M. leprae rpoB gene
C	15	16.8	84.0	3474	23	AAO51357	Enterococcus faeca
C	16	16.8	84.0	3624	23	AAO52892	Enterococcus faeca
C	17	16.8	84.0	9179	20	AAI13246	C. glutamicum SRT
C	18	15.4	77.0	612	22	AAI71082	C. glutamicum codin
C	19	15.4	77.0	1344	22	AAH68297	Human immune syste
C	20	15.4	77.0	6275	24	ABJ32551	C. glutamicum codin
C	21	15.4	77.0	309400	22	AAH68534	Arabidopsis thalia
C	22	15.2	76.0	1446	21	AAI42071	Arabidopsis thalia
C	23	15.2	76.0	2853	23	ABJ12631	Drosophila melanog
C	24	15.2	76.0	3276	23	ABJ02493	Drosophila melanog
C	25	15.2	76.0	4505	21	AAI15009	Nucleotide sequenc
C	26	15.2	76.0	5574	23	ABJ02492	Drosophila melanog
C	27	15.2	76.0	7243	23	ABJ02521	Drosophila melanog
C	28	15.2	76.0	8193	23	ABJ12630	Drosophila melanog
C	29	15.2	76.0	21748	23	ABJ02520	Drosophila melanog
C	30	15.2	76.0	27426	23	AAO59541	Protonibacterium
C	31	15.2	76.0	4403765	22	AAI199683	Mycobacterium tube
C	32	15	75.0	27	17	AAI09670	Mycobacterium tube
C	33	14.8	74.0	822	23	AAO54258	Pseudomonas aerugi
C	34	14.8	74.0	894	23	AAO54258	Pseudomonas aerugi
C	35	14.8	74.0	1167	22	AAI81355	Quorum sensing con
C	36	14.8	74.0	2176	15	AAO57017	PKC nu. Bos tauru
C	37	14.4	72.0	1014	22	AAH65487	C. glutamicum codin
C	38	14.4	72.0	1086	23	AAO53170	DNA encoding novel
C	39	14.4	72.0	1086	23	AAO53170	DNA encoding novel
C	40	14.4	72.0	1578	21	AAO48875	Arabidopsis thalia
C	41	14.4	72.0	1579	21	AAO48875	Arabidopsis thalia
C	42	14.4	72.0	2660	23	ABJ10327	Drosophila melanog
C	43	14.4	72.0	3342	23	ABJ12342	Drosophila melanog
C	44	14.4	72.0	3362	23	ABJ17225	Drosophila melanog
C	45	14.4	72.0	3632	23	ABJ13365	Drosophila melanog

ALIGNMENTS

RESULT 1

AAA49824 standard; DNA: 20 BP.

AAA49824:

25-SEP-2000 (first entry)

Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.

Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

ss.

Mycobacterium tuberculosis.

WO200036142-A1.

22-JUN-2000.

10-DEC-1999: 99MO-CA01177.

11-DEC-1998: 98US-0111794.

(VIST-) VISIBLE GENETICS INC.

Shipman R;

WPI: 2000-431611/37.

Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 4; 43pp; English.

XX The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp

CC 2611-2592). It is used with the forward primer given in AAA49823

CC and with the sequencing primers given in AAA49825 and AAA49826 for the

CC detection and analysis of antibiotic resistance-associated mutations

CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing

CC primers (see AAA49823-62) have been developed for the detection and

CC analysis of antibiotic resistance-associated mutations in defined

CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA

CC (chlorfloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and

CC characterization of *M. tuberculosis* present in a sputum sample.

CC The method involves performing a sequencing procedure, with or

CC without prior amplification, to detect the presence of *M.*

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12

CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If *M. tuberculosis* is detected, a second sequencing procedure is

CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-inducing mutations. Genotypic

CC tests are rapid, sensitive and accurate providing information as to

CC antibiotic treatment options.

XX

SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20

|||||

DB 1 tacggcggttcgatgaacc 20

RESULT 2

AAA49826

ID AAA49826 standard; DNA; 20 BP.

XX

AC AAA49826;

XX

DT 25-SEP-2000 (first entry)

XX

DE *Mycobacterium tuberculosis* rpoB gene sequencing primer rpoB-3s.

XX

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

KW ss.

XX

OS *Mycobacterium tuberculosis*.

XX

PN WO200036142-A1.

XX

PD 22-JUN-2000.

XX

PF 10-DEC-1999; 99WO-CA01177.

XX

PR 11-DEC-1998; 98US-0111794.

XX

PA (VISI-) VISIBLE GENETICS INC.

XX

PI Shipman R;

XX

DR WPI; 2000-431611/37.

XX

PT Method for the detection and characterization of *Mycobacterium*

XX tuberculosis with antibiotic resistance in a sample -

PS Claim 4; Page 5; 43pp; English.

XX

XX The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp

CC 2611-2592). It is used with the forward primer given in AAA49825 and

CC with the amplification primers given in AAA49823 and AAA49824 for the

CC detection and analysis of antibiotic resistance-associated mutations

CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing

CC primers (see AAA49823-62) have been developed for the detection and

CC analysis of antibiotic resistance-associated mutations in defined

CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA

CC (chlorfloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and

CC characterization of *M. tuberculosis* present in a sputum sample.

CC The method involves performing a sequencing procedure, with or

CC without prior amplification, to detect the presence of *M.*

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12

CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If *M. tuberculosis* is detected, a second sequencing procedure is

CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-inducing mutations. Genotypic

CC tests are rapid, sensitive and accurate providing information as to

CC antibiotic treatment options.

XX

SQ Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20

|||||

DB 1 tacggcggttcgatgaacc 20

RESULT 3

AAO61457/C

ID AAO61457 standard; DNA; 432 BP.

XX

AC AAO61457;

XX

DT 17-MAY-1994 (first entry)

XX

DE *M. tuberculosis* rpoB gene fragment.

XX

KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;

KW mutant; ss.

XX

OS *Mycobacterium tuberculosis*.

XX

PN WO9322454-A.

XX

PD 11-NOV-1993.

XX

PF 30-APR-1993; 93WO-EP01063.

XX

PR 17-SEP-1992; 92FR-0011098.

XX

PR 30-APR-1992; 92US-0875940.

XX

PR 14-AUG-1992; 92US-0929206.

XX

PR 16-APR-1993; 93FR-0004545.

XX

PA (ASSI-) ASSISTANCE PUBLIQUE.

PA (INSP) INST PASTEUR.

PA (MEDI-) MEDICAL RES COUNCIL.

PA (UYBE-) UNIV BERNE.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;

XX Young D, Zhang Y;

XX

DR WPI; 1993-366812/46.

XX

P-PSDB; AAR51372.

XX

PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in katC, rpoB or rpsL genes
PS Example 2; Fig 13; 97pp; English.
XX PCR amplification was used to obtain rpoB genes from rifampicin-
CC resistant Mycobacterium lepre strains. A comparison with the
CC sequence of the rpoB gene from sensitive strains (AA051332) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from M.tuberculosis (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taaggcgcttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA; 480 BP.
XX
AC AAA49863;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene (rifampin resistance).
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; ss.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*cag- a
FT /*note= "primer of AAA49823"
FT primer_bind 372..391
FT /*cag- b
FT /*note= "primer of AAA49824"

MO200036142-A1.
XX
PN 22-JUN-2000.
XX
PD 10-DEC-1999; 99WO-CA01177.
XX
PF 11-DEC-1998; 98US-0111794.
XX
PR (VIST-) VISIBLE GENETICS INC.
XX
PA Shipman R;
XX
PI WPI; 2000-431611/37.
XX
DR Method for the detection and characterization of Mycobacterium
PT tuberculosis with antibiotic resistance in a sample -
XX
PS Disclosure; Page 5; 43pp; English.
XX
CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of rpoB (rifampin), katC (isoniazid), oxyR-aphc PR
CC (isoniazid), mbdA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taaggcgcttcgatgaacc 20
|||||
DB 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620 BP.
XX
AC AAT29126;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from Mycobacterium tuberculosis.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
XX Escherichia; Saccharomyces; Campylobacter; Mycobacterium; Shigella;
XX Staphylococcus; Identification; detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
FH Key Location/Qualifiers
FT primer_bind complement(41..60)
FT /*cag- a
FT /*note= "primer of AAA49823"
FT primer_bind 372..391
FT /*cag- b
FT /*note= "primer of AAA49824"

WO9615267-A1.
XX
PN 09-NOV-1995; 95WO-US14673.
XX
PF 30-AUG-1995; 95US-0520946.
XX
PR 09-NOV-1994; 94US-0337164.
XX
PR 09-MAR-1995; 95US-0402601.
XX
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg WC, Olive DM;
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavage (RTM) BN enzyme,
CC Thermus aquaticus DNA polymerase, Thermus thermophilus DNA
CC polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera *Campylobacter*,
CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the *Mycobacterium tuberculosis* rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

SO

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaaccc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA; 620 BP.
XX
AC AAT29124;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment from *Mycobacterium tuberculosis*.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
KM *Staphylococcus*; Identification; detection; ds.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM,
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera *Campylobacter*,
CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the *Mycobacterium tuberculosis* rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

SO

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaaccc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA; 620 BP.
XX
AC AAT29125;
XX
DT 02-DEC-1996 (first entry)
XX
DE rpoB gene fragment (mutant) from *Mycobacterium tuberculosis*.
XX
KM p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KM *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
KM *Staphylococcus*; Identification; detection; ds.
XX
OS *Mycobacterium tuberculosis*.
XX
PN WO9615267-A1.
XX
PD 23-MAY-1996.
XX
PF 09-NOV-1995; 95WO-US14673.
XX
PR 30-AUG-1995; 95US-0520946.
PR 09-NOV-1994; 94US-0337164.
PR 09-MAR-1995; 95US-0402601.
PR 07-JUN-1995; 95US-0484956.
XX
PA (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
PI Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;
PI Oldenburg MC, Olive DM,
XX
DR WPI; 1996-259862/26.
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
PS Example 33; Page 305-306; 433pp; English.
XX
CC Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

RESULT 9
AAH51976/C
ID AAH51976 standard; DNA: 3519 BP.
XX
AC AAH51976;
XX
DT 04-SEP-2001 (first entry)
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
KM Drug target; growth; organism viability; characterisation; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200135317-A1.
XX
PD 17-MAY-2001.
XX
PF 13-NOV-2000; 2000WO-US31152.
XX
PR 12-NOV-1999; 99US-0165086.
XX
PR 12-NOV-1999; 99US-0165124.
XX
PR 01-FEB-2000; 2000US-0179531.
XX
PA (RBC) UNIV CALIFORNIA.
XX
PI Eisenberg D, Rotstein SH, Marcotte EM.
XX
DR WPI: 2001-329193/34.
DR P-PSDB; AAG81125.
XX
XX
PT Identifying nucleotide or polypeptide sequence for use as drug target.
PT Involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
PS Disclosure; Page 68-69; 207pp; English.
XX
CC This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
SQ Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other:

Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
Db 1529 TACGGCGTTTCGATGAACCC 1510
|||||

RESULT 10
AAH02079/C
ID AAH02079 standard; DNA: 3534 BP.
XX
AC AAH02079;
XX
DT 24-JUL-2001 (first entry)

XX
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
KM Species specific; genus specific; family specific; probe: detection;
KM identification; algal; archaeal; bacterial; fungal; parasitica;
KM microorganism; diagnosis; translation elongation factor Tu; toxin;
KM translation elongation factor G; RecA recombinase; resistance;
KM catalytic subunit of proton-translocating ATPase; antimicrobial;
KM vaccine; primer; ds.
XX
XX
OS Mycobacterium tuberculosis.
XX
PN WO200123604-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-CA01150.
XX
PR 28-SEP-1999; 99CA-2283458.
XX
PR 19-MAY-2000; 2000CA-2307010.
XX
PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
XX
PI Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI Picard FJ, Roy PH;
XX
DR WPI: 2001-245006/25.
XX
XX
PT Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitica species in a test sample -
XX
PS Disclosure; Page 1478-1479; 1580pp; English.

CC The present invention describes a method for generating a repertoire of
CC nucleic acids of tuf, fus, atpd and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitica
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitica species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (I) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
CC which are given in the exemplification of the present invention.
XX
SQ Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other:

Query Match 100.0%; Score 20; DB 22; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
Db 1547 TACGGCGTTTCGATGAACCC 1528
|||||

RESULT 11

```

AAAT4651/C
ID AAA74651 standard; DNA: 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
XX rifampin resistance; mutation detection; ds.
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US30377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
XX particularly for detecting rifampin resistance in Mycobacterium
XX tuberculosis -
XX
PS Example 1; Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match          100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||

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PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
XX 22-APR-1999; 99US-0296894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
XX Mycobacterium, comprising detecting mutations in a gene and relating
XX them to drug resistance -
XX
PS Example 1; Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such as rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match          100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
DB 2122 TACGGCGTTTCGATGAACCC 2103
|||||

```

```

RESULT 12
ID AAA89994/C
XX AAA89994 standard; DNA: 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
XX RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX

```

```

RESULT 13
ID AAT12096
XX AAT12096 standard; DNA: 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic; resistance; spectrum; gene; mycobacterium;
XX determination; amplification; tuberculosis; rpoB; fragment;
XX primer; differential; hybridisation; pattern; rifampicin;
XX rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelincx L, Portals F;

```

PI Rossau R;
 XX WPI: 1996-040250/04.
 DR
 XX
 PT Probes and primers for determ. of antibiotic resistance spectrum of
 PT Mycobacterium, opt. coupled with species identification - from
 PT different patterns of hybridisation with rpoB gene
 XX
 PS Claim 22: Page 39: 69pp; English.
 CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
 CC determined by amplifying the relevant part of the antibiotic
 CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
 CC amplified using the primer set AAT12091-98, hybridising it with at
 CC least 1 rpoB gene probe, detecting the hybrids formed and
 CC interpreting the ARS, and opt. the spp., from the differential
 CC hybridisation patterns. The method is partic. useful for the
 CC detection of rifampicin and/or rifabutin resistance in M. leprae
 CC or M. tuberculosis, and mycobacterial spp. identification. The
 CC method is rapid and reliable and provides simultaneous determ.
 CC of ARS and spp. identity.
 SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;
 OY Query Match 95.0%; Score 19; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 1 tacggcggttcgatgaacc 19
 1 tacggcggttcgatgaacc 19
 RESULT 14
 ID AAO51532/C
 AC AAO51532 standard; DNA: 3447 BP.
 XX
 AC AAO51532;
 DT 17-MAY-1994 (first entry)
 XX
 DE M.leprae rpoB gene.
 XX
 KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
 KW mutant; ss.
 XX
 OS Mycobacterium leprae.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..3447
 FT /*tag= a
 FT /note= "rifampicin-sensitive; in resistant
 strains the Ser codon (TCG at
 nucleotides 1273-1275) is often mutated
 to a Phe, Met or esp. Leu codon"
 FT
 XX W09322454-A.
 PN
 XX
 XX 11-NOV-1993.
 PD
 XX 30-APR-1993; 93WO-EP01063.
 PF
 XX 17-SEP-1992; 92FR-0011098.
 PR 30-APR-1992; 92US-0875940.
 PR 14-AUG-1992; 92US-0929206.
 PR 16-APR-1993; 93FR-0004545.
 XX
 PA (ASSI-) ASSISTANCE PUBLIQUE.
 PA (INSP) INST PASTEUR.
 PA (MEDI-) MEDICAL RES COUNCIL.
 PA (UYBE-) UNIV BERNE.
 PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX
 PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
 PI Young D, Zhang Y;
 XX
 DR WPI: 1993-368812/46.
 DR P-PSDB; AAR43671.
 XX
 PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
 PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
 PT by detecting mutation in katC, rpoB or rpsL genes
 XX
 PS Example 2: Fig 12; 97pp; English.
 CC PCR amplification was used to obtain rpoB genes from rifampicin-
 CC resistant Mycobacterium leprae strains. A comparison with the
 CC sequence of the rpoB gene from sensitive strains (AAO51532) revealed
 CC mutations in the region encoding amino acids 400-450. A common
 CC mutation seen in resistant strains occurs at codon 425 where Ser is
 CC substituted, most frequently by Leu.
 CC
 SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;
 OY Query Match 92.0%; Score 18.4; DB 14; Length 3447;
 Best Local Similarity 95.0%; Pred. No. 3;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1454 TACGGGTGTTGATGAACCC 1435
 1 tacggcggttcgatgaacc 20
 1454 TACGGGTGTTGATGAACCC 1435
 RESULT 15
 ID AAS51357/C
 AC AAS51357 standard; DNA: 3474 BP.
 XX
 AC AAS51357;
 DT 13-FEB-2002 (first entry)
 XX
 DE Enterococcus faecalis DNA for cellular proliferation protein #134.
 XX
 KW Antisense; ds; prokaryotic cellular proliferation gene;
 KW antibiotic; antibacterial; drug design.
 XX
 OS Enterococcus faecalis.
 XX
 PN W0200170955-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 21-MAR-2001; 2001WO-US09180.
 PF
 XX 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PA
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 DR WPI: 2001-611495/70.
 DR P-PSDB; AAU33498.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Claim 27: Seq ID No 3939; 51pp; English.

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:38 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

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Perfect score: 20
Sequence: 1 tacggcgttcgatgaacc 20

Scoring table:
IDENTITY-NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_sy:*
13:	gb_un:*
14:	gb_vl:*
15:	em_da:*
16:	em_fun:*
17:	em_hum:*
18:	em_ln:*
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31:	em_htg_inv:*
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33:	em_htggo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C	1	20	100.0	432	1	MSGRIFFNAP	L05910	Mycobacteri
C	2	20	100.0	432	6	AR067448	AR067448	Sequence
C	3	20	100.0	620	6	AR062056	AR062056	Sequence
C	4	20	100.0	620	6	AR062057	AR062057	Sequence
C	5	20	100.0	620	6	AR062058	AR062058	Sequence
C	6	20	100.0	620	6	AR062059	AR062059	Sequence
C	7	20	100.0	620	6	AR062060	AR062060	Sequence
C	8	20	100.0	620	6	AR062061	AR062061	Sequence
C	9	20	100.0	705	1	AF060353	AF060353	Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128	Sequence
C	11	20	100.0	970	6	I50706	I50706	Sequence
C	12	20	100.0	3534	6	AX111339	AX111339	Sequence
C	13	20	100.0	3853	1	MTU12205	U12205	Mycobacteri
C	14	20	100.0	5084	1	MSGRPOB	L27989	Mycobacteri
C	15	20	100.0	19352	1	AE006964	AE006964	Mycobacte
C	16	20	100.0	19770	1	MTG1376	Z95972	Mycobacte
C	17	18.4	92.0	626	1	AF060295	AF060295	Mycobacte
C	18	18.4	92.0	703	1	AF060349	AF060349	Mycobacte
C	19	18.4	92.0	705	1	AF060279	AF060279	Mycobacte
C	20	18.4	92.0	705	1	AF060290	AF060290	Mycobacte
C	21	18.4	92.0	705	1	AF060293	AF060293	Mycobacte
C	22	18.4	92.0	705	1	AF060297	AF060297	Mycobacte
C	23	18.4	92.0	705	1	AF060299	AF060299	Mycobacte
C	24	18.4	92.0	705	1	AF060300	AF060300	Mycobacte
C	25	18.4	92.0	705	1	AF060325	AF060325	Mycobacte
C	26	18.4	92.0	705	1	AF060326	AF060326	Mycobacte
C	27	18.4	92.0	705	1	AF060327	AF060327	Mycobacte
C	28	18.4	92.0	705	1	AF060328	AF060328	Mycobacte
C	29	18.4	92.0	705	1	AF060329	AF060329	Mycobacte
C	30	18.4	92.0	705	1	AF060331	AF060331	Mycobacte
C	31	18.4	92.0	705	1	AF060351	AF060351	Mycobacte
C	32	18.4	92.0	705	1	AF060366	AF060366	Mycobacte
C	33	18.4	92.0	3316	1	AF172323	AF172323	Bacillus
C	34	18.4	92.0	3447	6	AR067447	AR067447	Sequence
C	35	18.4	92.0	37617	1	MLB1790G	Z14314	M.leprae ge
C	36	18.4	92.0	348950	1	MLEPRTN7	AL583923	Agrobacte
C	37	17.4	87.0	10909	1	AE007977	AE007977	Agrobacte
C	38	17.4	87.0	13047	1	AE009010	AE009010	Agrobacte
C	39	16.8	84.0	518	1	AF325874	AF325874	Staphyloc
C	40	16.8	84.0	643	1	AF060346	AF060346	Mycobacte
C	41	16.8	84.0	647	1	AF060350	AF060350	Mycobacte
C	42	16.8	84.0	652	1	AF060344	AF060344	Mycobacte
C	43	16.8	84.0	652	1	AF060364	AF060364	Mycobacte
C	44	16.8	84.0	705	1	AF060283	AF060283	Mycobacte
C	45	16.8	84.0	705	1	AF060285	AF060285	Mycobacte

ALIGNMENTS

RESULT	1	432 bp	DNA	linear	BCT 21-MAY-1993
MSGRIFFNAP/c	432 bp	DNA	linear	BCT 21-MAY-1993	
LOCUS	MSGRIFFNAP	432 bp	DNA	linear	BCT 21-MAY-1993
DEFINITION	Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.				
ACCESSION	L05910				
VERSION	L05910.1	GI:149991			
KEYWORDS	RNA polymerase beta-subunit; rifampicin resistance.				
SOURCE	Mycobacterium tuberculosis (strain H37)				
ORGANISM	Mycobacterium tuberculosis				
REFERENCE	1 (bases 1 to 432)				
AUTHORS	Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.				
TITLE	Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis				
JOURNAL	Antimicrob. Agents Chemother. 341, 647-650 (1993)				
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	/organism="Mycobacterium tuberculosis"				
	/strain="H37"				

CDS

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 /transl_table=11
 /product="RNA polymerase beta subunit"
 /protein_id="AAB59068.1"
 /db_xref="GI:149992"
 /translation="GNRLRTVGGELIONQIRVGSRMERYRMTTODVEAIPPTL
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 149
 variation /phenotype="rifampicin resistant in association with
 mutation 234 G"
 188 /replace="C"
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 191 /replace="C"
 variation /phenotype="rifampicin resistant in association with
 mutation 203 T"
 194 /replace="C"
 variation /phenotype="rifampicin resistant"
 203 /replace="T"
 variation /phenotype="rifampicin resistant"
 /replace="T"
 208..210
 variation /phenotype="rifampicin resistant"
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 232 /phenotype="rifampicin resistant"
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 /replace="g"
 247..248
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 /replace="g"
 variation /phenotype="rifampicin resistant"
 /replace="L"
 254 /phenotype="rifampicin resistant"
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 BASE COUNT 77 a 140 c 148 g 67 t
 ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
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 DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2
 AR067448/c 432 bp DNA linear PAT 29-SEP-1999
 LOCUS AR067448

DEFINITION Sequence 59 from patent US 5851763.
 ACCESSION AR067448
 VERSION AR067448.1 GI:5998670
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 BASE COUNT 77 a 139 c 149 g 67 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
 |||
 DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
 AR062056/c 620 bp DNA linear PAT 29-SEP-1999
 LOCUS AR062056
 DEFINITION Sequence 135 from patent US 5843669.
 ACCESSION AR062056
 VERSION AR062056.1 GI:5989747
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 BASE COUNT 103 a 202 c 214 g 101 t
 ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
 |||
 DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
 AR062057/c 620 bp DNA linear PAT 29-SEP-1999
 LOCUS AR062057
 DEFINITION Sequence 136 from patent US 5843669.
 ACCESSION AR062057
 VERSION AR062057.1 GI:5989748
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE

Unknown.
 Unclassified.
 1 (bases 1 to 620)
 Kaiser, M.W., Lyamichev, V. I. and Lyamichev, N.
 Cleavage of nucleic acid using thermostable methanococcus

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
SOURCE 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c AR062058 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 137 from patent US 5843669.
DEFINITION AR062058
ACCESSION AR062058
VERSION AR062058.1 GI:5989749
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
SOURCE 1..620
/organism="unknown"

BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059 AR062059 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 138 from patent US 5843669.
DEFINITION AR062059
ACCESSION AR062059
VERSION AR062059.1 GI:5989750
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
SOURCE 1..620
/organism="unknown"

BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 tacggcgcttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060 AR062060 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 139 from patent US 5843669.
DEFINITION AR062060
ACCESSION AR062060
VERSION AR062060.1 GI:5989751
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
SOURCE 1..620
/organism="unknown"

BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061 AR062061 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 140 from patent US 5843669.
DEFINITION AR062061
ACCESSION AR062061
VERSION AR062061.1 GI:5989752
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
SOURCE 1..620
/organism="unknown"

BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353/c AF060353 705 bp DNA linear BCT 15-MAY-1998
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene.
DEFINITION

partial cds.
ACCESSION AF060353
VERSION AF060353.1 GI:3133464
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 705)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniwski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic mycobacterium
DNA arrays
JOURNAL Genome Res. 8 (5), 435-448 (1998)
MEDLINE 98248685
REFERENCE 2 (bases 1 to 705)
AUTHORS Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniwski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J.
TITLE Direct Submission
JOURNAL Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA
FEATURES
source 1..705
/organism="Mycobacterium tuberculosis"
/strain="ATCC27294"
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/db_xref="taxon:1773"
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/transl_table=11
/product="RNA polymerase beta-subunit"
/protein_id="AAC38533.1"
/db_xref="GI:3133465"
/translation="QDEAITPQTLINIRPVAAIKFEFTSOLSPMDONPLSGLT
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LVGTGMLRAIIDAT"

BASE COUNT 117 a 227 c 250 g 111 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 331 TACGGCGTTTCGATGAACCC 312

RESULT 10
ARI49128 706 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 24 from patent US 6228575.
DEFINITION ARI49128
ACCESSION ARI49128
VERSION ARI49128.1 GI:15113719
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 706)
AUTHORS Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
Ghandour,G. and Wang,C.
TITLE Chip-based species identification and phenotypic characterization
of microorganisms
JOURNAL Patent: US 6228575-A 24 08-MAY-2001;
FEATURES Location/Qualifiers

source 1..706
/organism="unknown"
BASE COUNT 117 a 227 c 250 g 111 t 1 others
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 706;
Best Local Similarity 100.0%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGAACCC 313

RESULT 11
150706/c 970 bp DNA linear PAT 07-OCT-1997
LOCUS Sequence 1 from patent US 5643723.
DEFINITION 150706
ACCESSION 150706
VERSION 150706.1 GI:2472409
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 970)
AUTHORS Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmler,T.A., Roberts,G.D.
and Whelan,A.Christian.
TITLE Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
JOURNAL Patent: US 5643723-A 1 01-JUL-1997;
FEATURES Location/Qualifiers
source 1..970
/organism="unknown"

BASE COUNT 182 a 302 c 330 g 156 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.5; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
AX111339 3534 bp DNA linear PAT 30-APR-2001
LOCUS Sequence 2072 from Patent WO0123604.
DEFINITION AX111339
ACCESSION AX111339
VERSION AX111339.1 GI:13927631
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 3534)
AUTHORS Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2072 05-APR-2001;
FEATURES Infectio Diagnostic (I.D.I.) INC. (CA)
source Location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
/db_xref="taxon:1773"

BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgagcttcgatgaacc 20
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Db 1547 TACGGCCTTCGATGAACCC 1528

RESULT 13
MTU12205/c 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE
ORGANISM Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The rpoB gene of Mycobacterium tuberculosis
Unpublished
2 (bases 1 to 3853)
Imboden, P.
Direct Submission
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
Location/Qualifiers
1. .3853
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576. .>3853
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576. .>3853
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/protein_id="AAA20242.2"
/db_xref="GI:7144499"

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TEKGTFLINTEYRKYVAVDSDEIYLLADEDEHVVAAQNSPIDADGRFEPVLRKAG
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IYKRLRGEPTKESAOITLLENFEKRYDLARVGRYKVKKILGLHVGPTSTLT
EEDVATIEYVLRHESQOTMIVPGVGEVPEPTDDIDHFGNRRLRTYGRKFAHSNGIC
MSMRERYRERMTTQDVEAITPOTLINIRPVAAIKFEGTSQLSQPMQDNNPISGLT
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FGFLETPYRKVVGVVSDGIVYLADDEHVVAAQNSPIDADGRFEPVLRKAG
EVEVYPSSEVDVNPROMVSVATAMIPELEHDAALGAMQAOAVLVRSKAG
LVNGGMLRAIDAATSSQESGVIEEVSADYITVMHNGTRRTYRMRKFAHSNGIC
ANOCPIYDAGRVAGOVYADGPTDGEALGNLVAIMPMEGHYEDAILISNLT
VEEDVLSIHIEHEIDARDTKLGAETITRIPNISDEVLAJDDERKIVRIGAEVRG
DILVGVTPKGETELTPEERLRLAIFEKAREVNDISLKVPHGSGVIGIRFESRD
EDELPAVNELVRYVAAKRIISDGLAGRHGKAGVIGKILPVEDMPFLADGPVVI
ILNTHGVRNNIGQILETHLGMCAHSGMKVDAKGVDMNAARLPDELLEAHNAIYS
TPVEDGAOEALGILSCTLPNRGDVLYADGAKAMFDGSGSPFPYPTVGYMYIM
KLHLVYDKIHARSTGYSMITQOPLGSKAOFGGRGEMECAMQAYGAAYTIQELL
TIKS"

BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 taccgagcttcgatgaacc 20
|||||
Db 2122 TACGGCCTTCGATGAACCC 2103

RESULT 14
MSGRPOB 5084 bp DNA linear BCT 13-SEP-1994
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB)
DEFINITION gene, complete cds and RNA polymerase beta'-subunit rpoC gene,
partial cds.
ACCESSION L27989.1 GI:468333
VERSION L27989.1
KEYWORDS RNA polymerase beta-subunit; rpoB gene.
SOURCE Mycobacterium tuberculosis (strain RV) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 5084)
Miller, L.P., Crawford, J.T. and Shinnick, T.M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
94304130
Location/Qualifiers
1. .5084
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/strain="RV"
/db_xref="taxon:1773"
1065. .4598
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/product="RNA polymerase beta-subunit"
/protein_id="AAA21416.1"
/db_xref="GI:468334"

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RDYGVGVIDRRKRPVTVLLKALGMSQIYERGFSEIMRSTLEKNDVTGDEALD
IYKRLRGEPTKESAOITLLENFEKRYDLARVGRYKVKKILGLHVGPTSTLT
EEDVATIEYVLRHESQOTMIVPGVGEVPEPTDDIDHFGNRRLRTYGRKFAHSNGIC
MSMRERYRERMTTQDVEAITPOTLINIRPVAAIKFEGTSQLSQPMQDNNPISGLT
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EVEVYPSSEVDVNPROMVSVATAMIPELEHDAALGAMQAOAVLVRSKAG
LVNGGMLRAIDAATSSQESGVIEEVSADYITVMHNGTRRTYRMRKFAHSNGIC
ANOCPIYDAGRVAGOVYADGPTDGEALGNLVAIMPMEGHYEDAILISNLT
VEEDVLSIHIEHEIDARDTKLGAETITRIPNISDEVLAJDDERKIVRIGAEVRG
DILVGVTPKGETELTPEERLRLAIFEKAREVNDISLKVPHGSGVIGIRFESRD
EDELPAVNELVRYVAAKRIISDGLAGRHGKAGVIGKILPVEDMPFLADGPVVI
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TPVEDGAOEALGILSCTLPNRGDVLYADGAKAMFDGSGSPFPYPTVGYMYIM
KLHLVYDKIHARSTGYSMITQOPLGSKAOFGGRGEMECAMQAYGAAYTIQELL
TIKSDDTVGRKIVETALVKGNIPEPGIPESFKVLLKELQSLNVEVLSDDGAIEL
REGDEDLERAAANIGILSNESASPEDLA"

gene 4641. .5084
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/protein_id="AAA21417.1"
/db_xref="GI:537608"

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BASE COUNT      969 a 1534 c 1691 g 890 t
ORIGIN

Query Match      100.0%; Score 20; DB 1; Length 5084;
Best Local Similarity 100.0%; Pred. No. 2,1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 lacggcggttcagatgaccc 20
|||||
Db 2611 TACGGCGTTCGATGATGCC 2592

RESULT 15
AE006964/c 19352 bp DNA linear BCT 27-APR-2001
LOCUS Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
DEFINITION complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS Mycobacterium tuberculosis CDC1551.
SOURCE Mycobacterium tuberculosis CDC1551.
ORGANISM Bacteria; Firmicutes; Actinobacteriinae; Mycobacteriaceae;
Actinomycetales; Corynebacteriales; Mycobacteriales;
Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 19352)
AUTHORS Flietschmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J.F., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Gill, J., Delcher, A., Uffetback, T., Weidman, J., Kouri, H.,
Gill, J., Mikula, A. and Bishai, W.
TITLE Whole genome comparison of Mycobacterium tuberculosis clinical and
laboratory strains
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 19352)
AUTHORS Flietschmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O.,
Peterson, J.F., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E.,
Kolonyak, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M.,
Gill, J., Delcher, A., Uffetback, T., Weidman, J., Kouri, H.,
Gill, J., Mikula, A. and Bishai, W.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
FEATURES
source
1. 19352
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/strain="CDC1551"
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PID:149992; identified by sequence similarity; putative"
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TERGTGTINGTERVVSQVLRSPGVFEDETIDSTDETLHSVYVPSRGAMLEDDVK
RDYVGVDIRKRPQPVYLKALGWTSEQIVERRGSEISMSTLEKNTYGTDEALD
IYKLRGPEPTKSAQTLLENLFEKERYDLARVGRYKVNKKLGLHVGHPITSTLT
EDVVATIEYLRHESQTYMYPGCVPEVDDIDHPCNRRLRTYGEGLIONDIRG
MSMRERVREMTTODVEAITPQTLNIRPVVAIKFEFTSQISQFMDNNPUSGLT
HKRLSLALGPGLSRERAGLEVDPVHPSHYGRMCPIETPGPNIGLIGLSVYARVP
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similarity; putative"
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/db_xref="GI:13880219"
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AAVEDODGELEAAROKLADLALEAAGAKADARRVRDGEERMOIRRAQRELD
LEDIMSTFTRKLAPKOLIVDENTYRELVDYGEVFGAMGAKESTLOKLENDIDGAS
LRDYIRNGKQKRLRLKRLKYAARQOQSNSPMGVLAQVPIIPPELRMNOIDGCR
FATSDINDLTRYRINNNRRLKRLIDGAPITVNNERMLQESVDALDFNGRGREYV
GPNRPLKRLSYDLNKKQGRFONLIGKRDVSGRSIVVGPOLKHLQCGPLMLME
LFPNFWKRLSYDLNKKQGRFONLIGKRDVSGRSIVVGPOLKHLQCGPLMLME
IOAFEPMLVEGKALIOHPLVCEAFNADPDGQAAVHPLSAEQAEARILMSSNNIL
SPASGRPLAMPRLDMVGTGLYLTVEVPDETGEPQASGHPPEVGVSSPPELMAADR
GVLSVAKITVITQRRPEVETAEELFGSHGRRPGPAMMAETTLGVMPELLPLCP
EVNKKQHKVQAAITINDLERIPMIVVAQVITVDLKDGFWARISGVATYSMAVLP
RKKEILDHYEERADKVEKQFQALNHDENELVETWATEVGEQALREVPDNP
IITVDSGATNGFTQTRLGAMKGLVTNPGREIPRPVKSFRGLVLEYFTINTGA
RKGLADTALRTAGSLTRLRLVDSQDVIYREHDCOTERGIVVLEAERAPDGLIRP
YIETSAVARTIGDAVDGANGVIVERGQDGEDEIDALLAAGITQYKVRSLVLCATST
GVATCYGRSMATGKAVDGCENAVGIAAOSIGPGTOLIRTPHOCGVRSGLDGLPR
VQELFERVPRGAPLADYVGRVLEDEGERTYITTYPPDDGGEVYIDKLSKQRLRY
FKHEDSERVLSQGDHVEVGOQLMESADHELVYQGVREYVILHREVQEVYRAQG
VSJHDKHIEVIVROMLRVYIIDSSTFELPGSLIDRAEEAENRVRVAGGPPAQR
PVLMMGTAKASLADSMLSAASFQETTRVLTDALINCRSDKLNGLKEVYITGLIPAGT
GINRYNIAVQPIEEARAAYTIPSYEDQYSPDFGATGAAPVLDYGVSVR"
complement(7691..8065)
/gene="MT0697"
complement(7691..8065)
/note="identified by Glimmer2; putative"
/transl_table=11
/codon_start=1
/product="hypothetical protein"
/protein_id="AAK4923.1"
/db_xref="GI:13880220"
/translation="MFDSAAATINPGHAMASAMERSGLLECVAGLEOAPGFEFTADKL
NPDGSSRRVRRROADGIGATVHERGGQSGQGVVQVRMHGFPALAMORLIHH
GEOTONRIAGAFVRVCVCSPT"
complement(8058..9972)
/gene="MT0698"
/note="This region contains an authentic frame shift and
is not the result of a sequencing artifact; identified by
Glimmer2; putative; conserved hypothetical protein,
authentic frameshift"
10167..10925
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10167..10925
/gene="MT0699"
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PF01261"
/codon_start=1
/transl_table=11
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/product="Ap endonuclease, family 2"
/protein_id="AAK44924.1"
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/translation="MLGSHVSPTDPLAAAEACADVQVIFLGPQSKAKRPDDAA
ALKATLPITVHAPYLIINLASANNRVRIPSKLIQETCAADIGAAVIVGHVAD
DNIDKGFQRMKRLDRLETEVPVLENTGADAMARRPOTILADVIDGTGIFC
LDTCHTWAGSALTDADRIKAITGRIDLVICNCSREAGSGRDRHNLGSGQIDPDL
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10957..11799
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sequence similarity; putative"
/codon_start=1
/transl_table=1
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/protein_id="AAK44925.1"
/db_xref="GI:13880222"
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SYRLKPVGLPSSAPLYVMLHGSGAKAERSYGMDELADSEKELVAYPDGVRAN
ANGGCGGRPARBEGVDIGVRAYVADIANNVSDPARVYTGMSNGAHSYTLACNT
SIFAIGVSGTQDPCQSPRPSVHIHGTADPLVRHGGPGAGFARIDGPVPDDL
AFMRVNRGALDITTEGPPVTSGATCADNRVYLLTVDDAHRMPSFATQTLWRF
AHR"

11859..13487
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11859..13487
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/note="similar to SP:P33224 GB:L20915 PID:457172
PID:457174 PID:537028; identified by sequence similarity;
putative"
/codon_start=1
/transl_table=1
/product="acyl-CoA dehydrogenase, putative"
/protein_id="AAK44926.1"
/db_xref="GI:13880223"
/translation="MSDTHVVTNOVPLENNYPASSPYLIALIOEGGOMGLDEVNEV
GATISGQAOQWGLADNRPIILHTHDAVGYRDEVEDEPAVHELMRATHGMAAP
WADRRPAHYRAKTSWYTERGHICPISMTYAVVPALRYNSELAAYEPLTSREY
DPELKPATTKAGITAGMSMTEKGGSDVRACTQATPADGSYSLTGKWTSAVMD
IFVLAQAPDLSCFLPRVLPDGTNRNMFQRLDKLGNHANSSEVEYDGAVALV
GEEGRGVPTIETNLTDLDCALGSAISMGTGLRAVHAQRAKAFGAYLIDPLMR
VLADLAVEAEATIVAMMAGATDNAAVNETEALLRIGLAAKRYWCKRSTAAAE
ALBCLGNGYVEDSGMRIVREARLMGWESGVSADLTRAMATPRACVEYFDEL
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FLATRLGQWGCAGTWPAGLDLAPILERALVKG"
13498..14436
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13498..14436
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/note="similar to GP:3885480; identified by sequence
similarity; putative"
/codon_start=1
/transl_table=1
/product="enoyl-CoA hydratase/isomerase family protein"
/protein_id="AAK44927.1"
/db_xref="GI:13880224"
/translation="MTHAIRPVDFDNLKTMTYEVTGRIARTTFNRPEKGAIIADTPL
ELSAVLRADLDPGVHIVILVSGREGFCAGFDLSAYEGSSGSGAGVQGTVLGKT
QAVNHLNPOPMIDYOMSRFVGFASLMHADKPTVVKIHGYCAGAGTDIALHADQ
VIAADDAKIGYPTRWGVPRAGVLAHRAKRLLEFTGDCITGAQAAMEGLAVEA
PEPADLDERFERLVARIALPVPVNOIWKLLANSLALDOGVATSRMSTVPDGAARRHT
PEGHAFVADAVEGFROAVRRDEPFQYGRQASRV"
14439..15161
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14439..15161
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/codon_start=1
/transl_table=1
/product="hypothetical protein"

Query Match 100.0%; Score 20; DB 1; Length 19352;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 tacggcgttcgatgaacc 20
|||||
Db 1709 TACGGCGTTTCGATGAACCC 1690

Search completed: August 7, 2002, 21:51:46
Job time: 23881 sec

0y	1	tacagtcggagcgtgac	19	
Db	103	TACGCTCGCGACGTATTC	85	
RESULT	5			
BE443802				
LOCUS				
DEFINITION	BE443802	422 bp	mRNA	linear
	WH11122_B06_C122S	wheat etiolated seedling root normalized cDNA		EST 25-JUL-2000
	library Triticum aestivum CDNA clone WH1122_B06_C12, mRNA			
	sequence.			
ACCESSION	BE443802			
VERSION	BE443802.1	GI:9443341		
KEYWORDS	EST.			
SOURCE	Bread wheat.			
ORGANISM	Triticum aestivum			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae			
	; Triticaceae; Triticum.			
	1 (bases 1 to 422)			
REFERENCE	Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han			
AUTHORS	,P.S., Hsja,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,			
	Rauscher,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.			
	The structure and function of the expressed portion of the wheat			
	genomes - Normalized root cDNA library			
	Unpublished (2000)			
JOURNAL	Contact: Olin Anderson			
COMMENT	US Department of Agriculture, Agriculture Research Service, Pacific			
	West Area, Western Regional Research Center			
	800 Buchanan Street, Albany, CA 94710, USA			
	Tel: 5105595773			
	Fax: 5105593818			
	Email: oanderson@wpv.usda.gov			
	Sequence have been trimmed to remove vector sequence and low			
	quality sequence with phred score less than 20			
	Seq primer: Stragene SK primer.			
FEATURES	Location/Qualifiers			
SOURCE	1..422			
	/organism="Triticum aestivum"			
	/cultivar="Chinese Spring"			
	/db_xref="taxon:4565"			
	/clone="WH1122_B06_C12"			
	/clone_1lb="Wheat etiolated seedling root normalized cDNA			
	library"			
	/tissue_type="Root"			
	/dev_stage="Five day old etiolated seedling"			
	/lab_host="E. coli DH10B"			
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid			
	phluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were			
	surface-sterilized, germinated and grown aseptically in			
	the dark at room temperature on filter paper with water,			
	nystratin and cefotaxime in covered crystallization			
	dishes. Roots were harvested. The tissue, total RNA, and			
	poly(A) RNA were prepared, a cDNA library was made in the			
	TJ Close lab (Choi, Close, Fenton) at the University of			
	California, Riverside. The cDNA clones were in vivo			
	excised to give phluescript phagemids before			
	normalization was carried out. The mass excision of			
	phagemid library and normalization were done in HT Nguyen			
	lab by D. Zhang at Texas Tech Unversity. Normalization			
	protocol used was that of Soares. Plasmid DNA			
	preparations and DNA sequencing were performed in the OD			
	Anderson lab (all other authors)."			
BASE COUNT	84 a	130 c	124 g	84 t
ORIGIN				
Query Match	85.0%;	Score 17;	DB 10;	Length 422;
Best Local Similarity	100.0%;	Pred. No. 9,2e+02;		
Matches	17;	Conservative 0;	Mismatches 0;	Indels 0;
		Gaps 0;		
	4	ggtcggcgagctgac	20	

Db	86	GGTCGGCAGCTGATCC	102
RESULT	6		
LOCUS	BE445100	544 bp	linear
DEFINITION	WHE1132_H08_P16S Wheat etiolated seedling root normalized cDNA library		EST 25-JUL-2000
ACCESSION	BE445100		
VERSION	BE445100		
KEYWORDS	BE445100.1	GI:9444655	
SOURCE	bread wheat.		
ORGANISM	Triticum aestivum		
REFERENCE	Enkariyoti; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae; Triticeae; Triticum.		
AUTHORS	1 (bases 1 to 544)		
TITLE	Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsila,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.B., Tong,J.C. and Zhang,D.		
JOURNAL	The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library		
COMMENT	Unpublished (2000)		
	Contact: Olin Anderson		
	US Department of Agriculture, Agriculture Research Service, Pacifica		
	West Area, Western Regional Research Center		
	800 Buchanan Street, Albany, CA 94710, USA		
	Tel: 5105595773		
	Fax: 5105595818		
	Email: oanderson@nps.usda.gov		
	Sequence have been trimmed to remove vector sequence and low		
	quality sequence with phred score less than 20		
	Seq primer: Stragene SK primer.		
FEATURES	location/qualifiers		
SOURCE	1..544		
	/organism="Triticum aestivum"		
	/cultivar="Chinese Spring"		
	/db_xref="taxon:4565"		
	/clone="WHE1132_H08_P16"		
	/clone_lib="Wheat etiolated seedling root normalized cDNA library"		
	/tissue_type="Root"		
	/dev_stage="Five day old etiolated seedling"		
	/lab_host="E. coli DH10B"		
	/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI. Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the T7 Close lab (Choi, Close, Fenton) at the university of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."		
BASE COUNT	121 a	173 c	132 g
ORIGIN			118 t
Query Match	85.0%;	Score 17;	DB 10; Length 544;
Best Local Similarity	100.0%;	Pred. No. 9.8e+02;	
Matches 17; Conservative	0;	Mismatches	0; Gaps 0;
Db	512	GGTCGGCAGCTGATCC	528

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RESULT 7
LOCUS BE444713
DEFINITION BE444713 558 bp mRNA linear EST 25-JUL-2000
WHE1137_H03_005ZS Wheat etiolated seedling root normalized cDNA
1 library Trilicium aestivum cDNA clone WHE1137_H03_005, mRNA
sequence.
ACCESSION BE444713
VERSION BE444713.1 GI:9444264
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Trilicium aestivum
REFERENCE Trilicium aestivum: Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triliceae; Trilicium.
1 (bases 1 to 558)
Anderson, O.D., Cho, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
Unpublished (2000)
JOURNAL Contact: Olin Anderson
COMMENT US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: andersonepw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stralagene SK primer.
Location/Qualifiers
1..558
/organism="Trilicium aestivum"
/cultivar="Chinese Spring"
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/clone_lib="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/seq_strategy="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystratin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
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BASE COUNT 122 a 180 c 134 g 122 t

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggtcgcgcagctgctgcc 20
|||||
DB 514 ggtcgcgcagctgctgcc 530

RESULT 8

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BE195103
LOCUS BE195103 610 bp mRNA linear EST 22-OCT-2001
DEFINITION HVSMEN0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEN0088E21f,
mRNA sequence.
ACCESSION BE195103
VERSION BE195103.3 GI:163221083
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
REFERENCE Hordeum vulgare: Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triliceae; Hordeum.
1 (bases 1 to 610)
Wing, R., Close, T.J., Kleinbols, A., Wise, R., Begum, D., Frisch, D., Yu
, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
, R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
Unpublished (2001)
JOURNAL On Jun 26, 2000 this sequence version replaced gi:13187931.
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu
Total hg bases = 238
Seq primer: AATTAACCTCCTCACTAAGCG
High quality sequence stop: 563.
Location/Qualifiers
1..610
/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEN0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
/notes="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI.
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million p1u were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders
see Close TJ, Wing R, Kleinbols A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"
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BASE COUNT 127 a 203 c 158 g 120 t

ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ggtcgcgcagctgattcc 20
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 Db 499 GGTGCGCAGCTGATCC 515

RESULT 9
 BE442518 658 bp mRNA linear EST 25-JUL-2000
 LOCUS WHE1101.H10.O1925 wheat etiolated seedling root normalized cDNA
 DEFINITION library triticum aestivum cDNA clone WHE1101.H10.O19, mRNA

ACCESSION BE442518
 VERSION BE442518
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Triticum.
 1 (bases 1 to 658)
 Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 , P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
 Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)

JOURNAL Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

Email: oanderson@wv.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stralagene SK primer.
 Location/Qualifiers

FEATURES

1. 658
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1101.H10.O19"
 /clone_1lb="Wheat etiolated seedling root normalized cDNA
 library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pluscript SK; Site.1: EcoRI; Site.2: XhoI. Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 Tj Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pluscript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 144 a 203 c 165 g 140 t

ORIGIN

Query Match 85.0%: Score 17: DB 10: Length 658;
 Best Local Similarity 100.0%: Pred. NO. 1e+03;
 Matches 17: Conservative 0: Mismatches 0: Indels 0: Gaps 0;
 QY 4 ggtcgcgcagctgattcc 20

Db 512 GGTGCGCAGCTGATCC 528
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RESULT 10
 BG299722 828 bp mRNA linear EST 17-OCT-2001
 LOCUS HVSMEa0021120f Hordeum vulgare seedling shoot EST library
 DEFINITION HVCdNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
 mRNA sequence.

ACCESSION BG299722
 VERSION BG299722
 KEYWORDS EST.
 SOURCE barley.
 ORGANISM Hordeum vulgare

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
 ; Triticeae; Hordeum.
 1 (bases 1 to 828)
 Wing, R., Close, T.J., Kleinof, A., Wise, R., Begum, D., Frisch, D., Yu
 , Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
 Fenton, R.D. and Main, D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex cold-stressed seedling shoot cDNA
 library

JOURNAL Unpublished (2001)
 Contact: Wing R
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293

Email: rwing@clemson.edu
 Total hg bases = 574
 Seq primer: AATTAACCCCTCCTAAGCG
 High quality sequence stop: 643.
 Location/Qualifiers

FEATURES

1. 828
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEa0021120f"
 /clone_1lb="Hordeum vulgare seedling shoot EST library
 HVCdNA0001 (Cold stress)"
 /tissue_type="Seedling shoot"
 /lab_host="TJc121"
 /note="Vector: LambdaZAP; Site.1: EcoRI; Site.2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50C for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give pluscript SK(+) cDNA
 phagemids. These steps were performed in the Tj Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
 , DNA sequencing and sequence analysis were performed at
 CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t

ORIGIN

Query Match 85.0%: Score 17; DB 10; Length 828;
Best Local Similarity 100.0%: Pred. No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gtcgcgcagcgtcatcc 20
|||||
Db 500 GTCGCGCAGCTCATCC 516

RESULT 11
BI188703/c
LOCUS
DEFINITION BI188703 419 bp mRNA linear EST 10-JUL-2001
d2e05fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone d2e05fs 5', mRNA
sequence.

ACCESSION BI188703 GI:14662382
VERSION BI188703
KEYWORDS
SOURCE
ORGANISM Fusarium sporotrichioides.
Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.
1 (bases 1 to 419)
Ren,Q., Tag,A., Peplow,A., Lal,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Other_ESTs: d2e05fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability included
is the best homolog from a blastx search of Genbank nr 04-09-01
73 2.2 g117799258|emb|CA890 (AL355752) putative integral
membrane protease
Seq primer: T3
High quality sequence stop: 107.
Location/Qualifiers
1..419
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_id="d2e05fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site.1: EcoRI; Site.2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT 117 a 106 c 117 g 79 t
ORIGIN

Query Match 84.0%: Score 16.8; DB 10; Length 419;
Best Local Similarity 90.0%: Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tacggtcgcagcgtcatcc 20
|||||
Db 114 TACGCTCGCAGCTCATCC 95

RESULT 12
BI1981973
LOCUS
DEFINITION BI1981973 606 bp mRNA linear EST 24-OCT-2001
f533f08.y1 zebrafish adult brain Danio rerio cDNA clone 5333151 5'
similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN ; , mRNA sequence.

ACCESSION BI1981973
VERSION BI1981973.1 GI:16371108
KEYWORDS
SOURCE zebrafish.
ORGANISM Danio rerio
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 606)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Rither,E.,
Kohn,S., Shu,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
and Wilson,R.
Washu Zebrafish EST Project 1998
Unpublished (1998)
Other_ESTs: f533f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@wustl.edu
CDNA Library Preparation: John Neal, CDNA Library Arrayed by:
Matthew Clark, DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
Resourcenzen@trumpfarmdatabank, Berlin, Germany (web address:
www.rzpd.de)
High quality sequence stop: 446.
Location/Qualifiers
1..606
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_id="5333151"
/clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
/lab_host="E. coli DH10B"
/note="Vector: pZIRPlox; Site.1: NotI; Site.2: SalI.
Original library was constructed in lambdaZIRPlox. Mass
excision of the cDNA library was performed to yield
pZIRPlox plasmids. Insert check was done in original
library."
BASE COUNT 209 a 133 c 139 g 125 t
ORIGIN

Query Match 84.0%: Score 16.8; DB 10; Length 606;
Best Local Similarity 90.0%: Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tacggtcgcagcgtcatcc 20
|||||
Db 452 TACGCTCGCAGCTGTTC 433

RESULT 13
BI1888442/c
LOCUS
DEFINITION BI1888442 640 bp mRNA linear EST 12-OCT-2001
Z6637-2-000197 zebrafish shield stage whole embryo cDNA library
MPMGp637 Danio rerio cDNA clone MPMGP637_18E17;MPMGp637E1718 5',
mRNA sequence.
ACCESSION BI1888442 GI:16095713
VERSION BI1888442
KEYWORDS zebrafish.
SOURCE Danio rerio
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 640)
AUTHORS Clark, M., Amstad, P., Hennig, S., Johnson, S. L. and Lehrach, H.
TITLE EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
JOURNAL Unpublished (2001)
COMMENT Contact: Hennig S
Laboraty 123, dept. Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innesstr. 63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 640.
FEATURES
source
1..640
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="MPMP637_18E17:MPMP637E1718"
/clone_1lb="Zebrafish shield stage whole embryo cDNA
library MPMP637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XL1 Blue MRP"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
BASE COUNT 209 a 152 c 139 g 139 t 1 others
ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 640;
Best Local Similarity 90.0%; Pred. No. 1.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 taaggtcggcagctgaccc 20
|||||
Db 541 TACGTCGGCAGCTGTAC 522
RESULT 14
AM502654 292 bp mRNA linear EST 01-MAR-2000
LOCUS AM502654
DEFINITION UI-HF-BRDP-a]x-b-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075813 5', mRNA sequence.
ACCESSION AM502654
VERSION AM502654.1 GI:7117309
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 292)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rtmail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 forward.
FEATURES
source
1..292
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075813"
/clone_1lb="NIH_MGC_52"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p77T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 51 a 84 c 105 g 52 t
ORIGIN
Query Match 82.0%; Score 16.4; DB 9; Length 292;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 acggtcggcagctgac 19
|||||
Db 46 ACGTCGCGCTGCTGATC 63
RESULT 15
AM501791 338 bp mRNA linear EST 01-MAR-2000
LOCUS AM501791
DEFINITION UI-HF-BRDP-a]m-g-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075260 5', mRNA sequence.
ACCESSION AM501791
VERSION AM501791.1 GI:7115654
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 338)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rtmail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 forward.
FEATURES
source
1..338
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075260"
/clone_1lb="NIH_MGC_52"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: p77T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
BASE COUNT 56 a 98 c 124 g 60 t
ORIGIN
Query Match 82.0%; Score 16.4; DB 9; Length 338;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 acggtcggcgaactgac 19
 |||||
 Db 46 ACGGTCGGCGCTCTGATC 63

Search completed: August 7, 2002, 21:15:21
 Job time: 22891 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:16 : Search time 146.61 Seconds
(Without alignments)
33.508 Million cell updates/sec

Title: US-09-786-105-2

Sequence: 1 tacggcgttcgatgacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/pdata/2/1na/5A.COMB.seq:*
2: /cgn2_6/pdata/2/1na/5B.COMB.seq:*
3: /cgn2_6/pdata/2/1na/6A.COMB.seq:*
4: /cgn2_6/pdata/2/1na/6B.COMB.seq:*
5: /cgn2_6/pdata/2/1na/PCrUS.COMB.seq:*
6: /cgn2_6/pdata/2/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	432	2	US-08-313-185-59 Sequence 59, Appl
2	20	100.0	432	3	US-09-082-614A-59 Sequence 59, Appl
3	20	100.0	620	2	US-08-757-653-135 Sequence 135, App
4	20	100.0	620	2	US-08-757-653-136 Sequence 136, App
5	20	100.0	620	2	US-08-757-653-137 Sequence 137, App
6	20	100.0	620	2	US-08-757-653-138 Sequence 138, App
7	20	100.0	620	2	US-08-757-653-139 Sequence 139, App
8	20	100.0	620	2	US-08-757-653-140 Sequence 140, App
9	20	100.0	706	4	US-08-797-812-24 Sequence 24, Appl
10	20	100.0	970	1	US-08-250-030-1 Sequence 1, Appl
11	20	100.0	970	5	PCT-US95-06790-1 Sequence 1, Appl
12	19	95.0	19	4	US-08-750-088A-71 Sequence 71, Appl
13	18.4	92.0	3447	4	US-08-313-185-57 Sequence 57, Appl
14	18.4	92.0	3447	3	US-09-082-614A-57 Sequence 57, Appl
15	15.8	79.0	1472	1	US-08-622-354-2 Sequence 2, Appl
16	15.8	79.0	2310	1	US-08-622-354-1 Sequence 1, Appl
17	15.2	75.0	4403765	4	US-09-103-840A-2 Sequence 2, Appl
18	15	75.0	27	1	US-08-250-030-9 Sequence 9, Appl
19	15	75.0	27	5	PCT-US95-06790-9 Sequence 9, Appl
20	14.2	71.0	1081	4	US-09-372-422A-33 Sequence 33, Appl
21	14.2	71.0	1153	4	US-09-372-448A-5 Sequence 5, Appl
22	14.2	71.0	2262	2	US-08-674-887A-5 Sequence 5, Appl
23	14.2	71.0	2262	3	US-08-951-844-5 Sequence 5, Appl
24	13.8	69.0	117	1	US-08-299-498A-59 Sequence 59, Appl
25	13.8	69.0	117	5	PCT-US95-10813-59 Sequence 59, Appl
26	13.8	69.0	776	4	US-09-372-422A-43 Sequence 43, Appl
27	13.8	69.0	1100	4	US-09-372-422A-47 Sequence 47, Appl

28	13.8	69.0	1176	3	US-08-911-853-34 Sequence 34, Appl
29	13.8	69.0	1176	4	US-09-479-409-34 Sequence 34, Appl
30	13.8	69.0	1176	4	US-09-479-453-34 Sequence 34, Appl
31	13.8	69.0	1375	4	US-09-372-422A-37 Sequence 37, Appl
32	13.8	69.0	1485	4	US-09-372-422A-39 Sequence 39, Appl
33	13.8	69.0	2394	3	US-09-027-064-1 Sequence 1, Appl
34	13.8	69.0	2394	4	US-09-271-815-1 Sequence 1, Appl
35	13.8	69.0	17612	3	US-08-911-853-29 Sequence 29, Appl
36	13.8	69.0	17612	4	US-09-479-409-29 Sequence 29, Appl
37	13.8	69.0	17612	4	US-09-479-453-29 Sequence 29, Appl
38	13.8	69.0	4403765	4	US-09-103-840A-2 Sequence 2, Appl
39	13.6	68.0	585	4	US-09-404-671-3 Sequence 3, Appl
40	13.6	68.0	686	4	US-09-372-422A-45 Sequence 45, Appl
41	13.6	68.0	699	4	US-08-998-416-705 Sequence 705, App
42	13.6	68.0	999	4	US-09-177-234-7 Sequence 7, Appl
43	13.6	68.0	1087	4	US-09-372-422A-29 Sequence 29, Appl
44	13.6	68.0	1209	1	US-08-314-309A-5 Sequence 5, Appl
45	13.6	68.0	1513	1	US-08-314-309A-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Tien, Amalia
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/C
Sequence 59, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Zhang, Douglas
APPLICANT: Huang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunnet
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356,0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 428 TACGGCGTTTCGATGAACCC 409

RESULT 3
US-08-757-653-135/C
Sequence 135, Application US/08757653
Patent No. 5843669

GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 4
US-08-757-653-136/C
Sequence 136, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-136

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
US-08-757-653-137/c
Sequence 137, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-137

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
US-08-757-653-138
Sequence 138, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-653-138

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
US-08-757-653-139
Sequence 139, Application US/08757653
Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Medlen & Carroll, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States Of America
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,653
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: FORS-02565
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 139:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-757-653-139

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgtttcgatgaacc 20
|||||
Db 325 TACGCGTTTCGATGAACCC 344

;; RESULT 8
;; US-08-757-653-140
;; Sequence 140, Application US/08/757653
;; Patent No. 5843669
;; GENERAL INFORMATION:
;; APPLICANT: Kaiser, Michael W.
;; APPLICANT: Lyamichev, Victor I.
;; APPLICANT: Lyamichev, Natasha
;; TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
;; TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
;; NUMBER OF SEQUENCES: 190
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Medlen & Carroll, LLP
;; STREET: 220 Montgomery Street, Suite 2200
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States Of America
;; ZIP: 94104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/757,653
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ingolia, Diane E.
;; REGISTRATION NUMBER: 40,027
;; REFERENCE/DOCKET NUMBER: FORS-02565

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 705-8410
;; TELEFAX: (415) 397-8338
;; INFORMATION FOR SEQ ID NO: 140:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 620 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-757-653-140

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgtttcgatgaacc 20
|||||
Db 325 TACGCGTTTCGATGAACCC 344

;; RESULT 9
;; US-08-797-812-24/C
;; Sequence 24, Application US/08/797812
;; Patent No. 6228575
;; GENERAL INFORMATION:
;; APPLICANT: Gingeras, Thomas A.
;; APPLICANT: Mack, David
;; APPLICANT: Chee, Mark S.
;; APPLICANT: Berne, Anthony J.
;; APPLICANT: Strayer, Aubert
;; APPLICANT: Ghandour, Ghassan
;; TITLE OF INVENTION: Chip-Based Species Identification and
;; TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/797,812
;; FILING DATE: 07-FEB-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/017,765
;; FILING DATE: 15-MAY-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/629,031
;; FILING DATE: 08-APR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/012,631
;; FILING DATE: 01-MAR-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/011,339
;; FILING DATE: 08-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Fitts, Renee A.
;; REGISTRATION NUMBER: 35,136
;; REFERENCE/DOCKET NUMBER: 16528X-018550
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-326-2400
;; TELEFAX: 415-326-2422
;; INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-797-812-24

Query Match 100.0%; Score 20; DB 4; Length 706;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 332 TACGGCGTTTCGATGAACCC 313

RESULT 10
US-08-250-030-1/c
Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin in Mycobacterial Cultures and in
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250.030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueeling, Ann M. 33,977
REGISTRATION NUMBER: 150.105US1
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-250-030-1

Query Match 100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 671 TACGGCGTTTCGATGAACCC 652

RESULT 11
PCT-US95-06790-1/c
Sequence 1, Application PC/TUS9506790

GENERAL INFORMATION:

APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105WO1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US95-06790-1

Query Match 100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
DB 671 TACGGCGTTTCGATGAACCC 652

RESULT 12
US-08-750-088A-71
Sequence 71, Application US/08750088A
Patent No. 6329138
GENERAL INFORMATION:
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: D.C.
COUNTRY: US
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657,0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-750-088A-71

Query Match 95.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 19
|||||
DB 1 TACGGCGTTTCGATGACCC 19

RESULT 13
US-08-313-185-57/c
Sequence 57, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356,0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57

Query Match 92.0%; Score 18.4; DB 2; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
|||||
DB 1454 TACGGCGTTTCGATGACCC 1435

RESULT 14
US-09-082-614A-57/c
Sequence 57, Application US/09082614A
Patent No. 6124098
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356,0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-082-614A-57

Query Match 92.0%; Score 18.4; DB 3; Length 3447;
Best Local Similarity 95.0%; Pred. No. 0.32;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 tacggcgcttcgatgaacc 20
|||||

Db 1454 TACGGTGTTCGATGACCC 1435

RESULT 15

US-08-622-354-2/C
Sequence 2, Application US/08622354
Patent No. 5827518
GENERAL INFORMATION:
APPLICANT: WEBB, Bruce A.
APPLICANT: CUI, Liwang
TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE
TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VA
COUNTRY: US
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,354
FILING DATE: 27-MAR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 434-061
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 684-1111
TELEFAX: (703) 684-1124
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1472 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1155
US-08-622-354-2

Query Match 79.0%; Score 15.8; DB 1; Length 1472;
Best Local Similarity 89.5%; Pred. No. 8;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 taagcgcttcgacgaacc 19
||||| ||||| ||||| ||||| |||||
Db 1105 TACGGGTTCGATGACCC 1087

Search completed: August 7, 2002, 21:54:21
Job time: 24016 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:38 : Search time 2167.9 Seconds
(Without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-3

Perfect score: 20
Sequence: 1 tacgtcgcgcgcgcgcgcgc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_da.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
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26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Match Length DB ID

Description

1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	6	MSGRIERNAP	MSGRIERNAP
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	150706	150706 Sequence
14	20	100.0	3534	6	MTU11339	MTU11339 Sequence
15	20	100.0	3853	1	MTU12205	MTU12205 Mycobacteri
16	20	100.0	5084	1	MSGRPOB	L27989 Mycobacteri
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTIC1376	295972 Mycobacteri
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18.4	92.0	25	6	AT7816	AT7816 Sequence
22	18.4	92.0	306	1	AF057456	AF057456 Mycobacte
23	18.4	92.0	306	1	AF057459	AF057459 Mycobacte
24	18.4	92.0	306	1	AF057460	AF057460 Mycobacte
25	18.4	92.0	306	1	AF057471	AF057471 Mycobacte
26	18.4	92.0	306	1	AF057473	AF057473 Mycobacte
27	18.4	92.0	306	1	AF057496	AF057496 Corynebact
28	18.4	92.0	306	1	AF173087	AF173087 Mycobacte
29	18.4	92.0	306	6	AR157005	AR157005 Sequence
30	18.4	92.0	306	6	AR157010	AR157010 Sequence
31	18.4	92.0	306	6	AR157011	AR157011 Sequence
32	18.4	92.0	306	6	AR157021	AR157021 Sequence
33	18.4	92.0	306	6	AR157024	AR157024 Sequence
34	18.4	92.0	306	6	AR157046	AR157046 Sequence
35	18	90.0	87	6	AX050338	AX050338 Sequence
36	17.4	87.0	306	1	AF057463	AF057463 Mycobacte
37	17.4	87.0	306	1	AF057466	AF057466 Mycobacte
38	17.4	87.0	306	1	AF057475	AF057475 Mycobacte
39	17.4	87.0	306	1	AF057480	AF057480 Mycobacte
40	17.4	87.0	306	1	AF057489	AF057489 Mycobacte
41	17.4	87.0	306	1	AF057492	AF057492 Mycobacte
42	17.4	87.0	306	1	AF057494	AF057494 Rhodococc
43	17.4	87.0	306	1	AF057495	AF057495 Nocardi
44	17.4	87.0	306	1	AF173084	AF173084 Mycobacte
45	17.4	87.0	306	1	AF173086	AF173086 Mycobacte

ALIGNMENTS

RESULT 1
AF057450 306 bp DNA linear BCT 17-SEP-1999
LOCUS Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial
DEFINITION
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS
SOURCE Mycobacterium africanum.
ORGANISM Mycobacterium africanum
Bacteria; Firmicutes; Actinobacteria; Actinobacteriidae;
Actinomycetales; Corynebacteriineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 306)
REFERENCE Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bal,G.H., Chae,G.T.,
AUTHORS Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE 99262756
PUBMED 10325313
REFERENCE Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bal,G.H.,
AUTHORS

TITLE Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES
source Location/Qualifiers
1.306
/organism="Mycobacterium africanum"
/strain="ATCC25420"
/db_xref="ATCC:25420"
/db_xref="taxon:33894"
<1..>306
/gene="rpoB"
<1..>306
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta"
/protein_id="A05514.1"
/db_xref="GI:5902488"
/translation="RTVGEIIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
VVAATKEPFGTSLSQPMQNNPLSGLTTHKRRLSALGPGLSRERAGLEVADVHPSH"

gene
CDS
Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctgcgcagctgattcc 20
|||||
Db 5 TACGCTGCGCAGCTGATCC 24

RESULT 2
AF057451 306 bp DNA linear BCT 17-SEP-1999
LOCUS Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
DEFINITION AF057451
ACCESSION AF057451.1 GI:5902489
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium bovis.
Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J Clin Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL 99262756
MEDLINE 10325313
PUBMED 2 (bases 1 to 306)
REFERENCE Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
AUTHORS Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
TITLE Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES
source Location/Qualifiers
1.306
/organism="Mycobacterium bovis"
/strain="ATCC19210"
/db_xref="ATCC:19210"
/db_xref="taxon:1765"
<1..>306
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<1..>306
/gene="rpoB"
/codon_start=3

/transl_table=11
/product="RNA polymerase beta"
/protein_id="A05515.1"
/db_xref="GI:5902490"
/translation="RTVGEIIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
VVAATKEPFGTSLSQPMQNNPLSGLTTHKRRLSALGPGLSRERAGLEVADVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctgcgcagctgattcc 20
|||||
Db 5 TACGCTGCGCAGCTGATCC 24

RESULT 3
AF057452 306 bp DNA linear BCT 17-SEP-1999
LOCUS Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
DEFINITION (rpoB) gene, partial cds.
ACCESSION AF057452
VERSION AF057452.1 GI:5902491
KEYWORDS
SOURCE
ORGANISM
Mycobacterium bovis BCG.
Mycobacterium bovis BCG.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
J Clin Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL 99262756
MEDLINE 10325313
PUBMED 2 (bases 1 to 306)
REFERENCE Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
AUTHORS Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
TITLE Direct Submission
Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES
source Location/Qualifiers
1.306
/organism="Mycobacterium bovis BCG"
/strain="French 1173P2"
/db_xref="taxon:33892"
<1..>306
/gene="rpoB"
<1..>306
/gene="rpoB"
/codon_start=3
/transl_table=11
/product="RNA polymerase beta"
/protein_id="A05516.1"
/db_xref="GI:5902492"
/translation="RTVGEIIONQIRVGSRMERVRERMTODVEAITPOTLINIRP
VVAATKEPFGTSLSQPMQNNPLSGLTTHKRRLSALGPGLSRERAGLEVADVHPSH"

BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacgctgcgcagctgattcc 20
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Db      5  TACGTCGGCGAGCTGATCC 24

RESULT  4
AF057453      306 bp  DNA      linear  BCT 17-SEP-1999
LOCUS      Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial
DEFINITION cds.
ACCESSION  AF057453
VERSION     AF057453.1  GI:5902493
KEYWORDS
SOURCE      Mycobacterium bovis BCG.
ORGANISM    Mycobacterium bovis BCG.
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium tuberculosis complex.
REFERENCE   1 (bases 1 to 306)
AUTHORS     Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y., and Kook,Y.H.
            Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
JOURNAL     J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE     99262756
PUBMED      10325313
REFERENCE   2 (bases 1 to 306)
AUTHORS     Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
            Direct Submission
            Submitted (06-Apr-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
            Korea

FEATURES
source      1..306
            /location=Qualifiers
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            /strain="Tokyo T172"
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            <1..>306
            /gene="rpoB"
            /codon_start=3
            /transl_table=11
            /product="RNA polymerase beta"
            /protein_id="AAD5517.1"
            /db_xref="GI:5902494"
            /translation="RTVGEILNQIRVGSRMERYRERMTTQDVEAITPOTLINIRP
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BASE COUNT  56 a      95 c      108 g      47 t

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  tacgctcgcgagctgattcc 20
        |||||||
Db      5  TACGTCGGCGAGCTGATCC 24

RESULT  5
AF057454      306 bp  DNA      linear  BCT 08-OCT-1999
LOCUS      Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial
DEFINITION cds.
ACCESSION  AF057454
VERSION     AF057454.1  GI:5902495
KEYWORDS
SOURCE      Mycobacterium tuberculosis.
ORGANISM    Mycobacterium tuberculosis.
            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium tuberculosis complex.

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REFERENCE   1 (bases 1 to 306)
AUTHORS     Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y., and Kook,Y.H.
            Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
JOURNAL     J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE     99262756
PUBMED      10325313
REFERENCE   2 (bases 1 to 306)
AUTHORS     Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
            Direct Submission
            Submitted (06-Apr-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
            Korea

FEATURES
source      1..306
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            /organism="Mycobacterium tuberculosis"
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BASE COUNT  56 a      95 c      108 g      47 t

ORIGIN
Query Match      100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  tacgctcgcgagctgattcc 20
        |||||||
Db      5  TACGTCGGCGAGCTGATCC 24

RESULT  6
ARI57003      306 bp  DNA      linear  PAT 08-AUG-2001
LOCUS      Sequence 2 from patent US 6242584.
DEFINITION  ARI57003
ACCESSION  ARI57003
VERSION     ARI57003.1  GI:15125707
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
            Unclassified.
REFERENCE   1 (bases 1 to 306)
AUTHORS     Kook,Y. and Kim,B.
            Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
            Patent: US 6242584-A 2 05-JUN-2001;
            Location/Qualifiers
            1..306
            /organism="unknown"

BASE COUNT  56 a      95 c      108 g      47 t

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  tacgctcgcgagctgattcc 20
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Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 7

LOCUS AR157007 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 6 from patent US 6242584.

ACCESSION AR157007

VERSION AR157007.1 GI:15125711

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y.-H. and Kim,B.-J.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of ipob gene

JOURNAL Patent: US 6242584-A 6 05-JUN-2001;

FEATURES

source Location/Qualifiers

1..306

/organism="unknown"

BASE COUNT 56 a 96 c 107 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcagctgattcc 20

|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 8

LOCUS AR157008 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 7 from patent US 6242584.

ACCESSION AR157008

VERSION AR157008.1 GI:15125712

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y. and Kim,B.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of ipob gene

JOURNAL Patent: US 6242584-A 7 05-JUN-2001;

FEATURES

source Location/Qualifiers

1..306

/organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcagctgattcc 20

|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 9

LOCUS AR157042 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 41 from patent US 6242584.

ACCESSION AR157042

VERSION AR157042.1 GI:15125746

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y. and Kim,B.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of ipob gene

JOURNAL Patent: US 6242584-A 41 05-JUN-2001;

FEATURES

source Location/Qualifiers

1..306

/organism="unknown"

BASE COUNT 56 a 95 c 108 g 47 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcagctgattcc 20

|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 10

LOCUS AR157051 306 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 50 from patent US 6242584.

ACCESSION AR157051

VERSION AR157051.1 GI:15125755

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 306)

AUTHORS Kook,Y. and Kim,B.

TITLE Method for identifying mycobacterial species by comparative sequence analysis of ipob gene

JOURNAL Patent: US 6242584-A 50 05-JUN-2001;

FEATURES

source Location/Qualifiers

1..306

/organism="unknown"

BASE COUNT 56 a 94 c 108 g 48 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;

Best Local Similarity 100.0%; Pred. No. 96;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcggcagctgattcc 20

|||||

Db 5 TACGGTCGGCAGCTGATCC 24

RESULT 11

LOCUS MSGRIPRNAP 432 bp DNA linear BCT 21-MAY-1993

DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.

ACCESSION L05910.1 GI:149991

VERSION RNA polymerase beta-subunit; rifampicin resistance.

KEYWORDS Mycobacterium tuberculosis (strain H37) DNA.

SOURCE Mycobacterium tuberculosis

ORGANISM Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacteriineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

REFERENCE Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.

AUTHORS Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis

TITLE tuberculosi

JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

FEATURES

source location/Qualifiers

1..432

/organism="Mycobacterium tuberculosis"

/strain="H37"

/db_xref="taxon:1773"

<1..>432

/codon_start=1

/transl_table=11

/product="RNA polymerase beta subunit"

/protein_id="AB59068.1"

/db_xref="GI:149992"

/translation="GNRRRLTVGELIQNIRVGSRMERVRREMTTQDVEATPQTLINIRPVAAIKKEFTQSOFMDQNNPLSGLHKRRRLSLGPGGSLSRERAGIEVRDYPHSHYCRMCPTEPECPNIGLISLVARVNPFCFTEPPYR"

variation /phenotype="rifampicin resistant in association with mutation 234 G"

188 /replace="c"

189 /phenotype="rifampicin resistant"

191 /replace="c"

191 /phenotype="rifampicin resistant in association with mutation 203 T"

194 /replace="c"

194 /phenotype="rifampicin resistant"

203 /replace="t"

203 /phenotype="rifampicin resistant"

208..210 /replace="t"

208 /phenotype="rifampicin resistant"

232 /replace="a"

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232 /replace="g"

232 /phenotype="rifampicin resistant"

233 /replace="a"

233 /phenotype="rifampicin resistant"

233 /replace="g"

233 /phenotype="rifampicin resistant"

234 /replace="c"

234 /phenotype="rifampicin resistant"

247..248 /replace="g"

247 /phenotype="rifampicin resistant"

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248 /replace="g"

248 /phenotype="rifampicin resistant"

254 /replace="t"

254 /phenotype="rifampicin resistant"

variation /phenotype="rifampicin resistant"

BASE COUNT 77 a 140 c 148 g 67 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 432;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20

|||||

Db 18 TACGTCGCGAGCTGATCC 37

RESULT 12

AR067448

LOCUS AR067448 432 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 59 from patent US 5651763.

AR067448

AR067448

AR067448.1 GI:5998670

VERSION

KEYWORDS

SOURCE

ORGANISM

Unknown.

Unclassified.

REFERENCE

1 (bases 1 to 432)

Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and Bodmer, T.

TITLE

Rapid detection of antibiotic resistance in mycobacterium tuberculosis

Patent: US 5651763-A 59 22-DEC-1998;

FEATURES

source location/Qualifiers

1..432

BASE COUNT 77 a 139 c 149 g 67 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;

Best Local Similarity 100.0%; Pred. No. 94;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20

|||||

Db 18 TACGTCGCGAGCTGATCC 37

RESULT 13

I50706

LOCUS I50706 970 bp DNA linear PAT 07-OCT-1997

DEFINITION Sequence 1 from patent US 5643723.

I50706

I50706

I50706.1 GI:2472409

VERSION

KEYWORDS

SOURCE

Unknown.

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 970)

Persing, D.H., Hunt, J.J., Young, K.K.Y., Peimlee, T.A., Roberts, G.D. and Whelan, A. Christian.

TITLE

Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens

Patent: US 5643723-A 1 01-JUL-1997;

JOURNAL

Location/Qualifiers

1..970

BASE COUNT 182 a 302 c 330 g 156 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgcagctgatcc 20

|||||

Db 261 TACGTCGCGAGCTGATCC 280

RESULT 14

AX111339

LOCUS AX111339 3534 bp DNA linear PAT 30-APR-2001

DEFINITION Sequence 2072 from Patent W00123604.

AX111339

AX111339

AX111339.1 GI:13927631

VERSION

KEYWORDS

SOURCE

Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
REFERENCE
AUTHORS Bergeron,M.G., Bolissnot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J. and Roy,P.H.
TITLE Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
JOURNAL Patent: WO 0123604-A 2072-05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES
Source location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="Rv"
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BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgagctgattcc 20
|||||
Db 1137 TACGTCGCGAGCTGATCC 1156
RESULT 15
MTU12205 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION
U12205
VERSION
U12205.1 GI:515684
KEYWORDS
SOURCE Mycobacterium tuberculosis.
ORGANISM Mycobacterium tuberculosis
REFERENCE
AUTHORS Imboden,P., Toller,R., Marchesi,F., Telenti,A., Bodmer,T.,
Cole,S., Schopfer,K. and Burkart,T.
TITLE The rpoB gene of Mycobacterium tuberculosis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3853)
AUTHORS Imboden,P.
TITLE Direct Submision
JOURNAL Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehstrasse 51, Berne,
3010, Switzerland
FEATURES
Source location/Qualifiers
1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
/db_xref="taxon:1773"
576..>3853
/gene="rpoB"
/gene="rpoB"
/codon_start=1
/transl_table=11
/product="RNA-polymerase beta subunit"
/protein_id="AA02042.2"
/db_xref="GI:7144499"
/translation="MLEGCIADSRQSKTAASPSRPOSSNNNSVPGANRYFAKL
REPLEVPGLDVQDSFEWLIGSPRMRESAARGDVNPGLEEVLYELSPIDFSG
MSLSFDPREFDKAPVDECKDKDMYAAPLFVTAPEINNNNGEIKSOTYFMGDFPM
TEKGTFLINGTERVVSOLYRSPGVFDETIKSTDKLASVYKVIIPSRGAMLEFDYDK
RDYGVGRIDRKRPQVTVILKALGWTSEQIVERFSGSEIKRSTLEKDNVTGIDEALLD
IYKLRPEPTKESAQTLLLENLFKEKRYDLARVGRYKVNKRLGLHVGEPITISFLT

EEDVATIEYLVRLHSGOTTMTVPGVEPVEETDDIDHFGNRRRLTVGELLIONQIRVG
MSMERVYREMRMTQDVEAITPQTLIRPVVAIKFEFTSOSQPMDONNPLSGLT
HKRRSLAGGGSLSRERAGLEVDPVHPSHGRMCPIETPGPNGLIGSLSVARVP
EGFLETPYRKVGVGVSVDGIVYLTADEPDHVVYVQANSPIDAGRPYEPVLRKAG
EVEYVSSEYDYMDSVFROMVSATAMIPFLEHDDANRALMGANMOQAVPLVRSAP
LVGTOMELRAIDAATSSSOESGVIEVSADYITVMDNCTRTYRMRKPARSNHGC
ANOCPIVDAGDRVACQVADGCTDGENALGNLVAIMPENHVEDAIILSNL
VEEDVLTSIHIEHEIDARDTKLGAETIPNDIPNISDEVLADDERGIVRIGAEVRDG
DILVGVTPKGETELPEERLLRAIFGEKAREVDTSIAKVPHGSGKVGIRVFSRED
EDELPGAVNELVRYVYVAAQKRKISDGKLAGRHGKNGVIGKILPYEDMPLADGTPNDI
ILNTHGVPRRMNIGQILETHHGMCAHSGKVDKAKVYPDMAARLPDELLERONAIYS
TPVFDGQENELGGLSCTLPNRDGDVLVDADGKAMLPDGRSGEPFPYPTVGVMTYM
KLHLIVDDKIHARSTGYSMTIQOPLGCKAOFGQRFGEHMCWAMQAVYGAAYTLQELL
TIKS"
BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggtcgcgagctgattcc 20
|||||
Db 1712 TACGTCGCGAGCTGATCC 1731

Search completed: August 7, 2002, 21:51:38
Job time: 23873 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:15:17 ; Search time 4103.44 Seconds
(without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 tacggcgttcgtatgaccc 20

Scoring table: IDENTITY_NUC

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estha:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	87.0	396	10	BF220419 NXCI_146-
2	17.4	87.0	399	10	BF169611 NXCI_125-
3	17.4	87.0	452	10	BG040291 NXCI_110-
4	17.4	87.0	539	9	AA556698 553 LobiO
5	17.4	87.0	545	10	BF777209 NXCI_066
6	17.4	87.0	234	10	W06754 SMEST0390 S
7	17.4	87.0	579	10	T24127 SMEST0325 S
8	16.8	84.0	277	9	AA734164 VS1912.r
9	16.4	82.0	576	10	BF252921 EST420184
10	16.4	82.0	624	10	BE896357 601439015
11	16.4	82.0	631	12	BH615799 BMBAC304F
12	16.4	82.0	961	12	AG141490 Pan trogl
13	15.8	79.0	213	9	AM064407 SP0996 KR
14	15.8	79.0	436	9	A1496312 sb05b08.y
15	15.8	79.0	582	12	AL147937 Anopheles
16	15.8	79.0	637	10	BG908684 Tair1170D
17	15.8	79.0	650	10	BG908616 Tair1169H

c 18	15.8	79.0	752	12	CNS03678	AL229661 Tetradon
c 19	15.8	79.0	775	12	A2125549	A2125549 OSJNB009
c 20	15.8	79.0	885	12	CNS0280Q	AL189251 Tetradon
c 21	15.8	79.0	913	10	BF204833	BF204833 601867133
c 22	15.8	79.0	1029	12	CNS0549K	AL320465 Tetradon
c 23	15.8	79.0	1411	10	B1663170	B1663170 603286791
c 24	15.6	78.0	885	12	CNS01K02	AL147715 Anopheles
c 25	15.4	77.0	248	10	BG140300	BG140300 EST480742
c 26	15.4	77.0	269	9	AV640876	AV640876 AV640876
c 27	15.4	77.0	384	10	BM077908	BM077908 PD21906.y
c 28	15.4	77.0	390	9	AV644609	AV644609 AV644609
c 29	15.4	77.0	467	12	CNS03FUV	AL242176 Tetradon
c 30	15.4	77.0	474	9	AV396989	AV396989 AV396989
c 31	15.4	77.0	489	9	AM618736	AM618736 EST320722
c 32	15.4	77.0	497	9	AV643117	AV643117 AV643117
c 33	15.4	77.0	508	9	AV642711	AV642711 AV642711
c 34	15.4	77.0	518	9	AV642141	AV642141 AV642141
c 35	15.4	77.0	531	9	AV642766	AV642766 AV642766
c 36	15.4	77.0	532	10	B1506216	B1506216 B170018A
c 37	15.4	77.0	536	12	A0783856	A0783856 HS_2001_A
c 38	15.4	77.0	548	12	A0497017	A0497017 HS_5197_B
c 39	15.4	77.0	566	9	AV631818	AV631818 AV631818
c 40	15.4	77.0	788	10	BE566696	BE566696 601339653
c 41	15.2	76.0	146	10	BM096759	BM096759 EBna07_SQ
c 42	15.2	76.0	200	10	BM098906	BM098906 EB105_SQ
c 43	15.2	76.0	205	12	A2577000	A2577000 06405_Sho
c 44	15.2	76.0	269	10	BF953380	BF953380 RC3-NN019
c 45	15.2	76.0	317	9	BB501888	BB501888 BB501888

ALIGNMENTS

RESULT 1
BF220419 396 bp mRNA linear EST 08-NOV-2000
LOCUS NXCI_146.A06.F NXCI (NsF Xylem Compression wood Inclined) Pinus
DEFINITION taeda cDNA clone NXCI_146.A06 5', mRNA sequence.

ACCESSION BF220419
VERSION BF220419.1 GI:11126551
KEYWORDS
SOURCE
ORGANISM

Pinus taeda

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Sederoff, R.
1 (bases 1 to 396)
Molecular Basis of Wood Formation in the Pine Megagenome
Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..396
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXCI_146.A06"
/clone_lib="NXCI (NsF Xylem Compression wood Inclined)"
/tissue_type="xylem"
/cell_type="Compression"
/dev_stage="juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site 1: Eco RI; Site 2: XhoI
The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of

all three genotypes was used for the library. oligo-dt primed cDNA was directionally cloned into the EcoRI-XhoI Bluescript SK vector arms. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTGGCAGCAG'.

BASE COUNT 71 a 84 c 122 g 110 t 9 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 396;
Best Local Similarity 94.7%; Pred. No. 71;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 acggcgttcgatgaacc 20
||||| |||||||||
Db 15 ACGGCGCTCGATGAACCC 33

RESULT 2
BF169611 399 bp mRNA linear EST 30-OCT-2000
LOCUS NCX1_125.C05.F NCX1 (Nsf Xylem Compression wood Inclined) Pinus
DEFINITION taeda cDNA clone NCX1_125.C05 5', mRNA sequence.
BF169611
VERSION BF169611.1 GI:11054228
KEYWORDS
SOURCE EST.
ORGANISM loblolly pine.
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Sederoft, R.
1 (bases 1 to 399)

REFERENCE
AUTHORS Molecular Basis of Wood Formation in the Pine Megagenome
TITLE Unpublished (2000)
JOURNAL Contact: Johnson, Arthur
COMMENT North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers

1..399
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NCX1_125.C05"
/clone_1lb="NCX1 (Nsf Xylem Compression wood Inclined)"
/tissue_type="Xylem"
/cell_type="Compression"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of
all three genotypes was used for the library. Oligo-dt
primed cDNA was directionally cloned into the EcoRI-XhoI
Bluescript SK vector arms. NOTE: The sequences contain a
'cDNA adapter' between the EcoRI site and the start of the
EST. The adapter sequence is 'AATTGGCAGCAG'."

BASE COUNT 71 a 84 c 121 g 121 t 2 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 399;
Best Local Similarity 94.7%; Pred. No. 72;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 acggcgttcgatgaacc 20
||||| |||||||||

Db 15 ACGGCGCTCGATGAACCC 33

RESULT 3
BG040291 452 bp mRNA linear EST 24-JAN-2001
LOCUS NXSL_110.F06.F NXSL (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
DEFINITION NXSL_110.F06.F NXSL (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
clone NXSL_110.F06 5', mRNA sequence.
BG040291
VERSION BG040291.1 GI:12482876
KEYWORDS
SOURCE EST.
ORGANISM loblolly pine.
Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
Sederoft, R.
1 (bases 1 to 452)

REFERENCE
AUTHORS Molecular Basis of Wood Formation in the Pine Megagenome
TITLE Unpublished (2000)
JOURNAL Contact: Johnson, Arthur
COMMENT North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.

FEATURES
source Location/Qualifiers

1..452
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="NXSL_110.F06"
/clone_1lb="NXSL (Nsf Xylem Side wood Inclined)"
/tissue_type="Xylem"
/cell_type="Side"
/dev_stage="Juvenile"
/lab_host="XLI-Blue"
/note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form side
wood by bending to a 45 degree angle and tying them to the
ground. Differentiating xylem was harvested from the sides
of the inclined stems, and a mixture of all three
genotypes was used for the library. oligo-dt primed cDNA
was directionally cloned into the EcoRI-XhoI Bluescript SK
vector arms. NOTE: The sequences contain a 'cDNA adapter'
between the EcoRI site and the start of the EST. The
adapter sequence is 'AATTGGCAGCAG'."

BASE COUNT 71 a 122 c 146 g 95 t 18 others

ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 452;
Best Local Similarity 94.7%; Pred. No. 74;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 acggcgttcgatgaacc 20
||||| |||||||||
Db 329 ACGGCGCTCGATGAACCC 347

RESULT 4
AA556698 539 bp mRNA linear EST 28-AUG-1998
LOCUS AA556698 553 loblolly pine CA Pinus taeda cDNA clone ICAB4c, mRNA sequence.
DEFINITION AA556698
ACCESSION AA556698.1 GI:3365713
VERSION
KEYWORDS EST.
SOURCE loblolly pine.
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 539)

REFERENCE

AUTHORS Allona, I., Quinn, M., Shoop, E., Swope, K., St. Cyr, S., Carls, J., Riedl, J., Retzel, E., Campbell, M.M., Sedoreff, R. and Whetten, R.W.
 TITLE Analysis of xylem formation in pine by cDNA sequencing
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (16), 9693-9698 (1998)
 MEDLINE 98356220
 COMMENT

Contact: Ross Whetten
 Forest Biotechnology Group
 North Carolina State University
 Dept. of Forestry, NC State University, 6113 Jordan Hall, Raleigh
 NC, 27695-8008
 Tel: 919-515-7800
 Fax: 919-515-7801
 Email: rosswhetten@unc.edu
 Seq primer: T3.

FEATURES
 source

1. .539
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="1CAB4G"
 /clone_lib="loblolly pine CA"
 /tissue_type="xylem"
 /lab_host="SOLR"
 /note="Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI;
 The result of subtraction of C library with N library.
 Immature xylem from the underside of inclined stems of
 differentiating compression wood was subtracted with
 immature xylem from the side of inclined stems of
 differentiating wood. A mixture of four genotypes were
 used. Oligo-dT primed cDNA was directionally cloned into
 the EcoRI-XhoI lambda-ZAP vector arms"
 BASE COUNT 102 a 120 c 156 g 150 t 11 others
 ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 539;
 Best Local Similarity 94.7%; Pred. No. 78;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgattgaacc 20
 ||||| ||||| ||||| |||||
 Db 145 ACGGCGCTTCGATTGAACCC 163

RESULT 5 545 bp mRNA linear EST 12-JAN-2001
 LOCUS BF777209
 DEFINITION NXSI_066_E05_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA
 clone NXSI_066_E05 5', mRNA sequence.
 ACCESSION BF777209
 VERSION BF777209.1 GI:12125109
 KEYWORDS EST.
 SOURCE loblolly pine.
 ORGANISM Pinus taeda
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
 REFERENCE 1 (bases 1 to 545)
 AUTHORS Sedoreff, R.
 TITLE Molecular Basis of Wood Formation in the Pine Megagenome
 JOURNAL Unpublished (2000)
 COMMENT Contact: Johnson, Arthur
 North Carolina State University
 Tel: 919 515 7800
 Fax: 919 515 7801
 Email: ajohnson@unc.edu
 Seq primer: T3.

FEATURES
 source

1. .545
 /organism="Pinus taeda"
 /strain="Coastal plain loblolly pine from North Carolina"
 /db_xref="taxon:3352"
 /clone="NXSI_066_E05"
 /clone_lib="NXSI (Nsf Xylem Side wood Inclined)"

/tissue_type="xylem"
 /cell_type="Side"
 /dev_stage="juvenile"
 /lab_host="XLI-Blue"
 /note="Vector: Bluescript SK; Site_1: Eco RI; Site_2: XhoI
 ; The library is from early (spring) wood, taken from
 three six-year old trees (three different genotypes), in
 the juvenile phase. These trees were induced to form side
 wood by bending to a 45 degree angle and tying them to the
 ground. Differentiating xylem was harvested from the sides
 of the inclined stems, and a mixture of all three
 genotypes was used for the library. oligo-dT primed cDNA
 was directionally cloned into the EcoRI-XhoI Bluescript SK
 vector arms. NOTE: The sequences contain a 'cDNA adapter'
 between the EcoRI site and the start of the EST. The
 adapter sequence is 'AATTCGGCACGAG'."
 BASE COUNT 92 a 142 c 167 g 132 t 12 others
 ORIGIN

Query Match 87.0%; Score 17.4; DB 10; Length 545;
 Best Local Similarity 94.7%; Pred. No. 78;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggcgcttcgattgaacc 20
 ||||| ||||| ||||| |||||
 Db 256 ACGGCGCTTCGATTGAACCC 274

RESULT 6 234 bp mRNA linear EST 01-JUL-1996
 LOCUS W06754/c
 DEFINITION SMeST0390 Schistosoma mansoni, adult worm, Gloria Franco
 Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence.
 ACCESSION W06754
 VERSION W06754.1 GI:1444974
 KEYWORDS EST.
 SOURCE Schistosoma mansoni.
 ORGANISM Schistosoma mansoni.
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 Strigeidida; Schistosomatidae; Schistosomatidae; Schistosoma.
 REFERENCE 1 (bases 1 to 234)
 AUTHORS Franco, G.R. and Pena, S.D.J.
 TITLE Franco, G.R. and Pena, S.D.J., Unpublished
 JOURNAL Unpublished (1996)
 COMMENT Contact: Franco G.R. and Pena S.D.J.
 Laboratorio de Genética-Bioquímica, Departamento de Bioquímica
 Imunologia
 Instituto de Ciências Biológicas, Universidade Federal de Minas
 Gerais
 Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
 Tel: (5531)4415611
 Fax: (5531)4415409
 Email: gfranco@mono.icb.ufmg.br
 Seq primer: M13 Forward.

FEATURES
 source

1. .234
 /organism="Schistosoma mansoni"
 /strain="NMRI"
 /db_xref="taxon:6183"
 /clone="SMPBE73"
 /clone_lib="Schistosoma mansoni, adult worm, Gloria
 Franco"
 /lab_host="DH10B, JM109"
 /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
 Total cellular RNA from male and female adult worms was
 extracted according to a modification (Puisant, C. and
 Houdebine, L. M. Biofeedback 8, 148-149, 1990) of the
 Guanidine Thiocyanate procedure (Chomczynski, P. and
 Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
 RNA was purified by Oligo dT column and cDNA was
 synthesized as described previously (Adams, M. D. et al.
 Nature Genet. 4, 373-389, 1993). cDNA was ligated to a

two fold molar excess of a NotI/HindIII digested plasmid DNA (Jafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "

BASE COUNT 49 a 84 c 66 g 33 t 2 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 234;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaa 17
|||||
Db 64 TACGGCGTTTCGATGAA 48

RESULT 7
T24127 579 bp mRNA linear EST 27-FEB-1995
LOCUS SMST0325 Schistosoma mansoni, adult worm, Gloria Franco
DEFINITION Schistosoma mansoni cDNA SMPBC65 3', mRNA sequence.
T24127
T24127.1 GI:529730
EST.
Schistosoma mansoni.
Schistosoma mansoni.
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
Strigoidae; Schistosomatidae; Schistosomatidae; Schistosoma.
1 (bases 1 to 579)
Franco, G.R., Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C.
and Pena, S.D.J.
Identification of new Schistosoma mansoni genes by the EST strategy
using a directional cDNA library
Gene 152, 141-147 (1995)
95137379
Contact: Franco G.R. and Pena S.D.J.
Laboratorio de Genética-Bioquímica, Departamento de Bioquímica
Imunologia
Instituto de Ciências Biológicas, Universidade Federal de Minas
Gerais
Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010
Tel: (3531)4415611
Fax: (3531)4415409
Email: gfranco@mono.icb.ufmg.br
Seg primer: M13 Forward.
Location/Qualifiers
1..579
/organism="Schistosoma mansoni"
/strain="NMRI"
/db_xref="taxon:6183"
/clone="SMPBC65"
/clone.lib="Schistosoma mansoni, adult worm, Gloria
Franco"
/lab_host="DH10B, JM109"
/note="Vector: BA vector. Site.1: NotI; Site.2: HindIII;
total cellular RNA from male and female adult worms was
extracted according to a modification (Pissant, C. and
Houdeline, L. M. Biofeedback 8, 148-149, 1990) of the
Guandine thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by oligo dt column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
two fold molar excess of a NotI/HindIII digested plasmid
DNA (Jafmid BA vector, a phagemid derived from pEMBL,
Adams, M. D. et al. Nature Genet. 4, 373-389, 1993) and
electroporated into E. coli strain DH10B (BRL). The

library was amplified and further selected for clones
containing long inserts (>500 bp) by purification of the
plasmid DNA from a fragment of a 1% low-melting-point
agarose gel, containing the smear of the library and
electroporation into DH10B cells. "

BASE COUNT 102 a 206 c 179 g 88 t 4 others

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 579;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaa 17
|||||
Db 75 TACGGCGTTTCGATGAA 59

RESULT 8
AA734164 277 bp mRNA linear EST 07-JAN-1998
LOCUS V519g12.r1 Barstead mouse irradiated colon MPLRB7 Mus musculus cDNA
DEFINITION (MOUSE); mRNA sequence.
AA734164
AA734164.1 GI:2755831
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 277)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:619998
Trace considered overall poor quality
Seg primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..277
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1138726"
/clone.lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
/note="Vector: p7T73D-Pac (Pharmacia) with a modified
polylinker. Site.1: EcoRI; Site.2: NotI; Tissue obtained
from 8 week old mouse. Colon was harvested 72 hours after
irradiation with 1400 Gy. 1st strand cDNA was primed
with a Not I - oligo(dT) primer
(5'-TGTTCGATCTGAGTGGACGCCCGCTTTTCTTTTCTTTTCTTTTCTTTT
T3'1); double-stranded cDNA was ligated to Eco RI
adaptors (AATTCGATCTTG), digested with Not I and cloned
into the Not I and Eco RI sites of the modified p7T73
vector. Library constructed by Bob Barstead. "

FEATURES
source

BASE COUNT 64 a 59 c 92 g 62 t

ORIGIN

Query Match 84.0%: Score 16.8; DB 9; Length 277;
Best Local Similarity 90.0%: Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 tagcgcttcgatgaaccc 20
||||| ||||||| |||||
Db 47 TACGGCATTTCGATGACACC 66

RESULT 9
BF252921/c 576 bp mRNA linear EST 15-NOV-2001
LOCUS BF252921
DEFINITION BF252921 Coccidioides immitis spherule cDNA library Coccidioides
immitis cDNA clone C1ABC49 5' sequence, mRNA sequence.
ACCESSION BF252921
VERSION BF252921.1 GI:16933064
KEYWORDS EST.
SOURCE Coccidioides immitis.
ORGANISM Coccidioides immitis.
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE 1 (bases 1 to 576)
AUTHORS Gardner,M.J. and Kirkland,T.
TITLE Generation of ESTs from Coccidioides immitis spherule cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Location/Qualifiers
1..576
/organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="C1ABC49"
/clone_lib="Coccidioides immitis spherule cDNA library"
/dev_stage="spherule"
/lab_host="SOLR"
/note="Vector: pluescript SK(-); Site_1: EcoRI; Site_2:
XhoI"

BASE COUNT 113 a 186 c 176 g 101 t

ORIGIN

Query Match 82.0%: Score 16.4; DB 10; Length 576;
Best Local Similarity 94.4%: Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cgagcgttcgatgaaccc 20
||||| ||||||| |||||
Db 241 CGCGCTGTCGATGACACC 224

RESULT 10
BE896357 624 bp mRNA linear EST 20-OCT-2000
LOCUS BE896357
DEFINITION 601439015F1 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:3924266 5',
mRNA sequence.
ACCESSION BE896357
VERSION BE896357.1 GI:10360678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC/DCFT/DP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LLM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers
1..624
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: PCMV-SPORE6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

BASE COUNT 155 a 209 c 150 g 110 t

ORIGIN

Query Match 82.0%: Score 16.4; DB 10; Length 624;
Best Local Similarity 94.4%: Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 cgagcgttcgatgaaccc 20
||||| ||||||| |||||
Db 580 CGCGCTTTCGATGACACC 597

RESULT 11
BH615799 631 bp DNA linear GSS 28-JAN-2002
LOCUS BH615799
DEFINITION BMAC304F01SP6_P5U Brugia malayi genomic Bac library 3 Brugia
malayi genomic, DNA sequence.
ACCESSION BH615799
VERSION BH615799.1 GI:18380487
KEYWORDS GSS.
SOURCE Brugia malayi.
ORGANISM Brugia malayi.
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
REFERENCE 1 (bases 1 to 631)
AUTHORS Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Foster
J., Guiliiano,D., Slatko,B. and Blaxter,M.
TITLE Genome survey sequences from the human parasitic nematode Brugia
malayi
JOURNAL Unpublished (2000)
COMMENT Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
3JF, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by the
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAEB, University of Edinburgh,
Edinburgh, UK.
Seq primer: SP6 (ATTAGTCACTATAG)
Class: BAC ends.
Location/Qualifiers
1..631
/organism="Brugia malayi"

/strain="TRS"
/db_xref="taxon:6279"
/clone_lib="Brugia malayi Genomic Bac Library 3"
/sex="Mixed (male and female)"
/issue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/note="Vector: pBAC3.6; Site:1: BamH I; Brugia malayi genomic DNA was partially cleaved with Sau3A I and size fractionated. 7,392 clones were generated with mean insert size ~48 kbp. The library was constructed by Claire Whitton, Baxter Nematode Genetics Lab, University of Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing Unit, The Sanger Centre, Cambridge, UK."

BASE COUNT 196 a 94 c 142 g 199 t

ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 631;
Best Local Similarity 94.4%; Pred. No. 2.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 accgagtttgatgaacc 19
|||||

Db 606 ACGGCGTTGATGATGCC 623

RESULT 12
AG141490 961 bp DNA linear GSS 08-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-001J13.TJ, genomic survey
DEFINITION
ACCESSION AG141490
VERSION AG141490.1 GI:16671168
KEYWORDS GSS: GSS (genome survey sequence).
SOURCE Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee Male BAC Library clone:RP43-001J13.TJ.
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Pan.
REFERENCE Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 961)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpanzee@gs.c.riken.go.jp, URL: http://hgp.gs.c.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
PRIMERS
Sequencing: TJ
LIBRARY
Vector : pBAC3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. 961
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J13.TJ"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
BASE COUNT 255 a 299 c 145 g 252 t 10 others
ORIGIN

Query Match 82.0%; Score 16.4; DB 12; Length 961;
Best Local Similarity 94.4%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 accgagtttgatgaacc 19
|||||

Db 746 ACGGCGTTGATGATGAACC 729

RESULT 13
AM064407/c 213 bp mRNA linear EST 07-DEC-2000
LOCUS SP0396 KRIIB Human CD4 intrathymic T-cell cDNA library Homo sapiens
DEFINITION
ACCESSION AM064407
VERSION AM064407.1 GI:8888344
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE Goh, S.-H., Park, J.-H., Lee, Y.-J., Lee, H.-G., Yoo, H.-S., Lee, I.-C., Park, J.-H., Kim, Y.-S. and Lee, C.-C.
TITLE Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development by cDNA sequencing analysis
JOURNAL Genomics 70 (1), 1-18 (2000)
MEDLINE 20541704
COMMENT Contact: Sung-Ho Goh
Genome Center
Korea Research Institute of Bioscience and Biotechnology
Oun-dong 52, Yu Sung-Gu, Daejeon 305-333, Republic of Korea
Tel: 82-42-860-4473
Fax: 82-42-860-4479
Email: gohsh@mail.kribd.re.kr
Seq primer: T7
High quality sequence stop: 213
POLYA-No.

FEATURES
source
1. 213
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KRIIB Human CD4 intrathymic T-cell cDNA library"
/issue_type="Thymus"
/cell_type="intrathymic T-cell"
/dev_stage="CD3+4+8- single positive stage"
/note="Vector: pGEM-T; cDNA was made from total cytoplasmic RNA of sorted human intrathymic CD3+4+8-T-cell, adaptor ligated, amplified with PCR, and cloned into pGEM-T vector."

BASE COUNT 41 a 59 c 72 g 40 t 1 others
ORIGIN

Query Match 79.0%; Score 15.8; DB 9; Length 213;
Best Local Similarity 89.5%; Pred. No. 4.3e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 accgagtttgatgaacc 20
|||||

Db 43 ACGGCGTTGATGATGAACC 25

RESULT 14
A1496312 436 bp mRNA linear EST 30-NOV-2001
LOCUS SP0508.Y1 Gm-cl1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl1004-7888 5' similar to TR:Q92388 Q92388 CRG1 GENE. ;, mRNA
DEFINITION
ACCESSION A1496312

VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
AI496312.1	GI:4397315	EST.	soybean. glycine max	1 (bases 1 to 436)	Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Corcell,V., Khanna,A., Bolla,B., Marret,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritters,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson, R.	Public Soybean EST Project	Unpublished (1999)	
			soybean. glycine max			Contact: Shoemaker R/Public Soybean EST Project		
			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eustosids I; Fabales; Fabaceae; Papilionoidae; Phaseoleae; Glycine.			Public Soybean EST Project		
						Washington University School of Medicine		
						4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
						Tel: 314 286 1800		
						Fax: 314 286 1810		
						Email: est@watson.wustl.edu		
						This clone is available through: ResGen, Invitrogen Corp. 2130		
						South Memorial Parkway Huntsville, AL 35801 For further information		
						call: (800)-533-4363 or contact via email: ccurresgen.com		
						Seq primer: -40RP from Gibco		
						High quality sequence stop: 386		
						POLYA-NO.		

FEATURES
SOURCE

BASE COUNT
ORIGIN

90 a 174 C 96 g 76 t

/*organism="Glycine max"
/*db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: gm-cl004-7888"
/clone.lib="Gm-cl004"
/tissue_type="root"
/lab_host="XL10-GOLD"
/note="Vector: pBluescript II XR; Site_1: EcoRI; Site_2:
XhoI; Root cDNA. The mRNA was isolated from entire roots
of 8 day old 'Williams' seedlings which were propagated on
paper towels with distilled water. Stratagene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First-strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stratagene's first-strand synthesis primer was used
(GACAGAGAGAGAGAGAGAGACTGACAG(T)-181. After
second-strand synthesis, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adaptors,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 500bp cutoff, using GldcoBRL Life
Technologies' cDNA Size Fractionation column. The column
eluent was then ligated into Stratagene's pBluescript II
XR Predigested vector (pBluescript II SK(+)) that had been
digested with EcoRI and XhoI, and phosphorylated). Both
the white and blue colonies appear to contain recombinant
plasmids with cDNA inserts. Blue colonies 9n-15) have been
sequenced, and possess putative cDNA inserts. This library
was constructed by Dr. Paul Kelm & Virginia H. Coryell,
Department of Biology, Box5640, Northern Arizona
University, Flagstaff, AZ 86011, Phone: 520-523-1078 (Dr.
Paul Kelm), 520-523-1372 (Virginia H. Coryell), Fax:
520-523-7500, email: paul.kelma@nau.edu,
virginia.coryell@nau.edu"

Query Match	79.08; Score 15.8; DB 9; Length 436;
Best Local Similarity	89.58; Pred. No. 5.3e+02;

	Matches	17; Conservative	0; Mismatches	2; Indels	0; Gaps
Qy	2	acgcgcgttcgaltgaacc	20		
Db	185	acgcgcgttcgaltgaacc	203		

RESULT 15

LOCUS	582 bp	DNA	Linear	GSS 12-JUN-2003
DEFINITION	Anopheles gambiae GSS SP6 end of clone 16E18 of NotreDamel library			

genomic survey sequence.
 accession number: AF147027

VERSION	AL14/937.1	GI:7006083
KEYWORDS	GSS.	

ORGANISM Anopheles gambiae
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:

freeflygata, neoptrera, enuoptrerygata, diptrera, nematocera, Culicoides: Anophel. 1 (base) 40. 500.

AUTHORS	Genoscope.
TITLE	Direct Submission

BP 191 91006 EVRY cedex - FRANCE (E-mail : segretef@genoscope.cns.fr)
- Web : www.genoscope.cns.fr

REFERENCE	AUTHORS
2 (pages 1 to 382)	Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.

JOURNAL Submitted (16-FEB-2000) **BMJ**, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France

COMMENT This clone is from an *A. gambiae* BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES	location/Qualifiers
source	1. .582

BASE COUNT	ORIGIN
160 a	124 c 136 g 153 t 9 others

Query Match 79.0%; Score 15.8; DB 12; Length 582;
Best Local Similarity 89.5%; Pred. No. 5.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0

Qy	2	acgcgcgttcgatgcaccc	20
Db	320	acgcgcgttcgatgcaccc	302

Search completed: August 7, 2002, 21:15:20
Job time: 22890 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 22:03:58 ; Search time 568.44 seconds
(without alignments)
60.408 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20
Sequence: 1 tacggcgttcgatgacc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_032802:*

- 1: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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- 19: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	20	AAA49824	Mycobacterium tube
2	20	100.0	20	AAA49826	Mycobacterium tube
3	20	100.0	432	AA061457	M. tuberculosis
4	20	100.0	480	AAA49863	Mycobacterium tube
5	20	100.0	620	AA729126	rpoB gene fragment
6	20	100.0	620	AA729124	rpoB gene fragment
7	20	100.0	620	AA729125	rpoB gene fragment
8	20	100.0	970	AA709676	Mycobacterium tube
9	20	100.0	3519	AAH51976	Mycobacterium tube

C	10	20	100.0	3534	22	AAH02079	Mycobacterium tube
C	11	20	100.0	3853	21	AAA74651	Mycobacterium tube
C	12	20	100.0	3853	21	AAA89994	M. tuberculosis
C	13	19	95.0	19	17	AA712096	M. tuberculosis
C	14	18.4	92.0	3447	14	AA051532	M. leprae
C	15	16.8	84.0	3474	23	AA551357	Enterococcus faeca
C	16	16.8	84.0	3624	23	AA552892	Enterococcus faeca
C	17	16.8	84.0	9179	20	AA513246	Enterococcus faeca
C	18	15.4	77.0	612	22	AA71082	C. glutamicum
C	19	15.4	77.0	1344	22	AAH68297	C. glutamicum
C	20	15.4	77.0	6275	24	ABL32551	Human
C	21	15.4	77.0	309400	22	AAH68534	C. glutamicum
C	22	15.2	76.0	1446	21	AA42071	Arabidopsis
C	23	15.2	76.0	2853	23	ABL12631	Drosophila
C	24	15.2	76.0	3276	23	ABL02493	Drosophila
C	25	15.2	76.0	4505	21	AAH15009	Nucleotide sequenc
C	26	15.2	76.0	5574	23	ABL02492	Drosophila
C	27	15.2	76.0	7243	23	ABL02521	Drosophila
C	28	15.2	76.0	8193	23	ABL12630	Drosophila
C	29	15.2	76.0	21748	23	ABL02520	Drosophila
C	30	15.2	76.0	27426	23	AA559541	Propionibacterium
C	31	15.2	76.0	4403765	22	AA199683	Mycobacterium tube
C	32	15	75.0	27	17	AA709670	Mycobacterium tube
C	33	14.8	74.0	822	23	AA554258	Pseudomonas aerugi
C	34	14.8	74.0	894	23	AA551512	Pseudomonas aerugi
C	35	14.8	74.0	1167	22	AA781355	Quorum sensing con
C	36	14.8	74.0	2176	15	AA057017	PKC nu.
C	37	14.4	72.0	1014	22	AAH65487	C. glutamicum
C	38	14.4	72.0	1086	23	AA593170	DNA encoding novel
C	39	14.4	72.0	1086	23	AA593247	Arabidopsis
C	40	14.4	72.0	1578	21	AA48875	Arabidopsis
C	41	14.4	72.0	1579	21	AA48875	Arabidopsis
C	42	14.4	72.0	2660	23	ABL10327	Drosophila
C	43	14.4	72.0	3342	23	ABL23542	Drosophila
C	44	14.4	72.0	3366	23	ABL17225	Drosophila
C	45	14.4	72.0	3632	23	ABL13365	Drosophila

ALIGNMENTS

RESULT 1	AAA49824	standard; DNA; 20 BP.
ID	AAA49824	
AC	AAA49824:	
XX		
DT	25-SEP-2000	(first entry)
XX		
DE	Mycobacterium tuberculosis	rpoB gene amplification primer rpoB-R.
XX		
KW	Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;	
KM	ss.	
XX		
OS	Mycobacterium tuberculosis.	
XX		
PN	WO200036142-A1.	
XX		
PD	22-JUN-2000.	
XX		
PF	10-DEC-1999;	99WO-CA01177.
XX		
PR	11-DEC-1998;	98US-0111794.
XX		
PA	(VISI-) VISIBLE GENETICS INC.	
XX		
PI	Shipman R;	
XX		
DR	WPI: 2000-431611/37.	
XX		
PT	Method for the detection and characterization of Mycobacterium	
XX	tuberculosis with antibiotic resistance in a sample -	

P5 Claim 4; Page 4; 43pp; English.

XX The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene amplification primer rpoB-R (bp

CC 2611-2592). It is used with the forward primer given in AAA49823

CC and with the sequencing primers given in AAA49825 and AAA49826 for the

CC detection and analysis of antibiotic resistance-associated mutations

CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing

CC primers (see AAA49823-92) have been developed for the detection and

CC analysis of antibiotic resistance-associated mutations in defined

CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA

CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and

CC characterization of *M. tuberculosis* present in a sputum sample.

CC The method involves performing a sequencing procedure, with or

CC without prior amplification, to detect the presence of *M.*

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12

CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If *M. tuberculosis* is detected, a second sequencing procedure is

CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-inducing mutations. Genotypic

CC tests are rapid, sensitive and accurate providing information as to

CC antibiotic treatment options.

XX

S0 Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20

Db 1 tacggcggttcgatgaacc 20

|||||

RESULT 2

AAA49826

ID AAA49826 standard; DNA: 20 BP.

XX

AC AAA49826;

XX

DT 25-SEP-2000 (first entry)

XX

DE *Mycobacterium tuberculosis* rpoB gene sequencing primer rpoB-3s.

XX

KW Antibiotic resistance; rpoB gene; rifampin resistance; primer;

KM 8S.

XX

OS *Mycobacterium tuberculosis*.

XX

PN WO200036142-A1.

XX

PD 22-JUN-2000.

XX

PF 10-DEC-1999; 99WO-CA01177.

XX

PR 11-DEC-1998; 98US-0111794.

XX

PA (VIST-) VISIBLE GENETICS INC.

XX

PI Shipman R;

XX

WP; 2000-431611/37.

DR

XX

PT Method for the detection and characterization of *Mycobacterium*

PT tuberculosis with antibiotic resistance in a sample -

XX

PS Claim 4; Page 5; 43pp; English.

XX

CC The present sequence is that of the *Mycobacterium tuberculosis*

CC rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp

CC 2611-2592). It is used with the forward primer given in AAA49825 and

CC with the amplification primers given in AAA49823 and AAA49824 for the

CC detection and analysis of antibiotic resistance-associated mutations

CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing

CC primers (see AAA49823-92) have been developed for the detection and

CC analysis of antibiotic resistance-associated mutations in defined

CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs

CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA

CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.

CC These primers can be used in a method for the detection and

CC characterization of *M. tuberculosis* present in a sputum sample.

CC The method involves performing a sequencing procedure, with or

CC without prior amplification, to detect the presence of *M.*

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12

CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If *M. tuberculosis* is detected, a second sequencing procedure is

CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-inducing mutations. Genotypic

CC tests are rapid, sensitive and accurate providing information as to

CC antibiotic treatment options.

XX

S0 Sequence 20 BP; 4 A; 6 C; 5 G; 5 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.32;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20

Db 1 tacggcggttcgatgaacc 20

|||||

RESULT 3

AAQ61457/GC

ID AAQ61457 standard; DNA: 432 BP.

XX

AC AAQ61457;

XX

DT 17-MAY-1994 (first entry)

XX

DE *M. tuberculosis* rpoB gene fragment.

XX

KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;

KM mutant; 8S.

XX

OS *Mycobacterium tuberculosis*.

XX

PN WO9322454-A.

XX

PD 11-NOV-1993.

XX

PF 30-APR-1993; 93WO-EP01063.

XX

PR 17-SEP-1992; 92FR-0011098.

XX

PR 30-APR-1992; 92US-0875940.

XX

PR 14-AUG-1992; 92US-0929206.

XX

PR 16-APR-1993; 93FR-0004545.

XX

PA (ASST-) ASSISTANCE PUBLIQUE.

PA (INSP) INST PASTEUR.

PA (MEDI-) MEDICAL RES COUNCIL.

PA (UYBE-) UNIV BERNE.

PA (UYPA-) UNIV CURIE PARIS VI P & M.

XX

PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;

PI Young D, Zhang Y;

XX

DR

XX

WP; 1993-368812/46.

DR

XX

P-PSDB; AAR51372.

PT Rapid detection of antibiotic resistance in *Mycobacterium* - esp.
PT Isoniazid, rifampicin or streptomycin resistance in tuberculosis
PT by detecting mutation in *katG*, *rpoB* or *rpsL* genes
XX
XX Example 2; Fig 13; 97pp; English.
XX
CC PCR amplification was used to obtain *rpoB* genes from rifampicin-
CC resistant *Mycobacterium lepreae* strains. A comparison with the
CC sequence of the *rpoB* gene from sensitive strains (AA051532) revealed
CC mutations in the region encoding amino acids 400-450. The corresp.
CC region was isolated from *M. tuberculosis* (AA061457). A common
CC mutation seen in resistant strains occurs at codon 425 where Ser is
CC substituted, most frequently by Leu.
XX
SQ Sequence 432 BP; 78 A; 139 C; 148 G; 67 T; 0 other;

Query Match 100.0%; Score 20; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 4
AAA49863/c
ID AAA49863 standard; DNA: 480 BP.
XX
XX AAA49863;
AC
XX
DT 25-SEP-2000 (first entry)
XX
DE *Mycobacterium tuberculosis rpoB* gene (rifampin resistance).
XX
XX Antibiotic resistance; *rpoB* gene; rifampin resistance; ss.
XX
OS *Mycobacterium tuberculosis*.
XX
XX
FH Key Location/Qualifiers
FH primer_bind /*cag- a complement(41..60)
FT /*cag- a /note= "primer of AAA49823"
FT primer_bind 372..391
FT /*cag- b /note= "primer of AAA49824"
FT /note= "primer of AAA49824"
XX
XX MO200036142-A1.
XX
XX 22-JUN-2000.
XX
XX 10-DEC-1999; 99WO-CA01177.
XX
XX 11-DEC-1998; 98US-0111794.
XX
XX (VIST-) VISIBLE GENETICS INC.
XX
XX Shipman R;
XX
XX WPI; 2000-431611/37.
XX
XX
PT Method for the detection and characterization of *Mycobacterium*
PT tuberculosis with antibiotic resistance in a sample -
XX
XX
PS Disclosure; Page 5; 43pp; English.
XX
XX The present sequence is that of the *Mycobacterium tuberculosis*
CC *rpoB* (rifampin resistance) gene (bp2161-2640). Amplification and
CC cycle sequencing primers (see AAA49823-62) are used for the detection
CC and analysis of antibiotic resistance-associated mutations in
CC defined regions of *rpoB* (rifampin), *katG* (isoniazid), *oxyR-aphC* PR
CC (isoniazid), *mabA* (isoniazid), *rpsL/s12* (streptomycin), 16S/rrs

CC (streptomycin), *embB* (ethambutol), *pncA* (pyrazinamide), *gyrA*
CC (ciprofloxacin) and 23S (azithromycin) genes of *M. tuberculosis*.
CC These primers can be used in a method for the detection and
CC characterization of *M. tuberculosis* present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of *M.*
CC *tuberculosis*, and if present to evaluate the *rpoB*, *katG*, *rpsL/s12*
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If *M. tuberculosis* is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
SQ Sequence 480 BP; 89 A; 153 C; 163 G; 75 T; 0 other;

Query Match 100.0%; Score 20; DB 21; Length 480;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcggttcgatgaacc 20
|||||
DB 451 TACGGCGTTTCGATGAACCC 432

RESULT 5
AAT29126/c
ID AAT29126 standard; DNA: 620 BP.
XX
XX AAT29126;
AC
XX
DT 02-DEC-1996 (first entry)
XX
XX
DE *rpoB* gene fragment (mutant) from *Mycobacterium tuberculosis*.
XX
XX p53; mutant; mutation; cleavage; nuclease; cleavage; *Thermus*;
XX *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
XX *Staphylococcus*; Identification; detection; ds.
XX
XX *Mycobacterium tuberculosis*.
XX
XX
OS
XX
XX MO9615267-A1.
XX
XX
PD 23-MAY-1996.
XX
XX
PF 09-NOV-1995; 95WO-US14673.
XX
XX 30-AUG-1995; 95US-0520946.
XX 09-NOV-1994; 94US-0337164.
XX 09-MAR-1995; 95US-0402601.
XX 07-JUN-1995; 95US-0484956.
XX
XX (THIR-) THIRD WAVE TECHNOLOGIES INC.
XX
XX Brow MAD, Dahlberg JE, Fors L, Helsler LM, Lyamichev VI;
XX Oldenburg MC, Olive DW;
XX
XX WPI; 1996-259862/26.
XX
XX
PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses
XX
XX
PS Example 33; Page 306; 43pp; English.
XX
XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of *Cleavage* (RPM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera *Campylobacter*,
CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the *Mycobacterium tuberculosis* rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451y and S456L mutations. The amplified
CC fragments are given in AAT29124 (wild type) and AAT29125-26
CC (mutant sequences).

XX Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AAT29124/c
ID AAT29124 standard; DNA: 620 BP.

XX AAT29124;

XX 02-DEC-1996 (first entry)

DE rpoB gene fragment from *Mycobacterium tuberculosis*.

XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
KW *Staphylococcus*; identification; detection; ds.

XX *Mycobacterium tuberculosis*.

XX WO9615267-A1.

XX 23-MAY-1996.

XX 09-NOV-1995; 95MO-US14673.

XX 30-AUG-1995; 95US-0520946.

XX 09-NOV-1994; 94US-0337164.

XX 09-MAR-1995; 95US-0402601.

XX 07-JUN-1995; 95US-0484956.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX Oldenburg MC, Olive DM;

XX WPI; 1996-259862/26.

PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses

XX Example 33; Page 305; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene; for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera *Campylobacter*,
CC *Escherichia*, *Mycobacterium*, *Salmonella*, *Shigella* and *Staphylococcus*.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the *Mycobacterium tuberculosis* rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451y and S456L mutations. The amplified
CC fragments are given in AAT29124 (wild type) and AAT29125-26
CC (mutant sequences).

XX Sequence 620 BP; 103 A; 202 C; 214 G; 101 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 7
AAT29125/c
ID AAT29125 standard; DNA: 620 BP.

XX AAT29125;

XX 02-DEC-1996 (first entry)

DE rpoB gene fragment (mutant) from *Mycobacterium tuberculosis*.

XX p53; mutant; mutation; cleavage; nuclease; cleavage; Thermus;
KW *Escherichia*; *Saccharomyces*; *Campylobacter*; *Mycobacterium*; *Shigella*;
KW *Staphylococcus*; identification; detection; ds.

XX *Mycobacterium tuberculosis*.

XX WO9615267-A1.

XX 23-MAY-1996.

XX 09-NOV-1995; 95MO-US14673.

XX 30-AUG-1995; 95US-0520946.

XX 09-NOV-1994; 94US-0337164.

XX 09-MAR-1995; 95US-0402601.

XX 07-JUN-1995; 95US-0484956.

PA (THIR-) THIRD WAVE TECHNOLOGIES INC.

XX Brow MAD, Dahlberg JE, Fors L, Heisler LM, Lyamichev VI;

XX Oldenburg MC, Olive DM;

XX WPI; 1996-259862/26.

PT Cleavage of nucleic acids to detect mutation(s) - allows detection
PT esp. in human p53 gene, to identify strains of microorganisms and
PT viruses

XX Example 33; Page 305-306; 433pp; English.

XX Cleavage of nucleic acids using an enzyme, especially a nuclease
CC selected from the group consisting of Cleavase (RTM) BN enzyme,
CC *Thermus aquaticus* DNA polymerase, *Thermus thermophilus* DNA
CC polymerase, *Escherichia coli* ExoIII and the *Saccharomyces cerevisiae*
CC Rad1/Rad10 complex. The nucleic acid substrate is preferably an
CC oligonucleotide containing a human p53 gene sequence or
CC alternatively, microbial gene sequences. Cleavage products are

CC compared to the cleavage products of reference gene sequences. The
CC method is used for detecting mutation in the human p53 gene: for
CC identifying strains of microorganisms, especially bacteria selected
CC from the group of members of the genera Campylobacter,
CC Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
CC The method may also be used for the identification of viruses,
CC especially hepatitis C virus (HCV) and simian immunodeficiency virus
CC (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp
CC region of the Mycobacterium tuberculosis rpoB gene, which, when
CC mutated is associated with rifampin resistance. The 620 bp region
CC amplified spans both the H451Y and S456L mutations. The amplified
CC fragments are given in AAT29124 (Wild type) and AAT29125-26
CC (mutant sequences).

XX
SQ Sequence 620 BP; 103 A; 201 C; 214 G; 102 T; 0 other;

Query Match 100.0%; Score 20; DB 17; Length 620;

Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
|||||
Db 296 TACGCGCTTCGATGAACCC 277

RESULT 8

AAT09676/c
ID AAT09676 standard; DNA: 970 BP.

XX
AC AAT09676;

DT 15-OCT-1996 (first entry)

XX
DE Mycobacterium tuberculosis rpoB gene DNA sequence.

XX
KM Tuberculosis: disease diagnosis; oligonucleotide; DNA primer; PCR;

XX
KM polymerase chain reaction; DNA amplification; rpoB locus; TB; ss.

XX
OS Mycobacterium tuberculosis.

XX
FH Key Location/Qualifiers

FT primer_bind 10..27

FT /*tag- a /note- "primer FENLEF"

FT primer_bind 226..243

FT /*tag- b /note- "primer DDIDL"

FT primer_bind 226..240

FT /*tag- c /note- "primer DDIDL"

FT primer_bind 338..364

FT /*tag- d /note- "primer rpo95"

FT primer_bind 348..373

FT /*tag- e /note- "primer rpo105"

FT primer_bind 334..373

FT /*tag- f /note- "primer KY290"

FT primer_bind 372..373

FT /*tag- g /note- "M. tuberculosis signature nucleotide"

FT primer_bind 433..434

FT /*tag- h /note- "M. tuberculosis signature nucleotide"

FT primer_bind 438

FT /*tag- i /note- "M. tuberculosis signature nucleotide"

FT primer_bind 468..469

FT /*tag- j /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- k /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

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FT primer_bind 486

FT /*tag- ea /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- eb /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- ec /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- ed /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- ee /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- ef /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- eg /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- eh /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- ei /note- "M. tuberculosis signature nucleotide"

FT primer_bind 486

FT /*tag- ej /note- "M.

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RESULT 9
AAH51976/c
ID AAH51976 standard; DNA: 3519 BP.
XX
XX AAH51976;
AC
XX 04-SEP-2001 (first entry)
DT
XX
DE Mycobacterium tuberculosis potential drug target gene SEQ ID 30.
XX
XX Drug target; growth; organism viability; characterisation; ds.
XX
XX Mycobacterium tuberculosis.
OS
XX WO200135317-A1.
XX
XX 17-MAY-2001.
PD
XX
XX 13-NOV-2000; 2000WO-US31152.
PF
XX 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Eisenberg D, Rotstein SH, Marcotte EM;
PI
XX WPI: 2001-329193/34.
DR
XX P-PSDB: AAG81125.
DR
XX
XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -
XX
XX Disclosure; Page 68-69; 207pp; English.
PS
XX
XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.
XX
XX Sequence 3519 BP; 675 A; 1081 C; 1183 G; 580 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 22; Length 3519;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
DB 1529 TACGGCGTTTCGATGACCC 1510
RESULT 10
AAH02079/c
ID AAH02079 standard; DNA: 3534 BP.
XX
XX AAH02079;
AC
XX
XX 24-JUL-2001 (first entry)
DT
```

```
XX
DE Mycobacterium tuberculosis nucleotide sequence SEQ ID NO:2072.
XX
XX Species specific; genus specific; family specific; probe; detection;
XX identification; algal; archaeal; bacterial; fungal; parasitical;
XX microorganism; diagnosis; translation elongation factor Tu; toxin;
XX translation elongation factor G; RecA recombinase; resistance;
XX catalytic subunit of proton-translocating ATPase; antimicrobial;
XX vaccine; primer; ds.
XX
XX Mycobacterium tuberculosis.
OS
XX WO200123604-A2.
XX
XX 05-APR-2001.
PD
XX
XX 28-SEP-2000; 2000WO-CA01150.
PF
XX 28-SEP-1999; 99CA-2283458.
PR 19-MAY-2000; 2000CA-2307010.
XX
XX (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
PA
XX
XX Bergeron MG, Boissinot M, Huletsky A, Menard C, Ouellette M;
PI
XX Ploard FJ, Roy PH;
PI
XX WPI: 2001-245006/25.
DR
XX
XX Nucleic acid sequences are used to generate universal probes and
PT primers which can be used to identify and detect the presence of algal,
PT archaeal, bacterial, fungal and parasitical species in a test sample -
PT
XX
XX Disclosure; Page 1478-1479; 1580pp; English.
PS
XX
XX The present invention describes a method for generating a repository of
CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes
CC and/or primers are derived. The method comprises amplifying the nucleic
CC acids of determined algal, archaeal, bacterial, fungal and parasitical
CC species with a combination of defined primer pairs. The method can be
CC used for producing probes and/or primers for detecting one or more
CC related microorganisms e.g. algae, archaea, bacteria, fungi and
CC parasites, for universal detection and for specific and ubiquitous
CC detection and identification of an algal, archaeal, bacterial, fungal
CC and parasitical species, genus, family and group. A nucleic acid (I)
CC obtained using the method of the invention can be used for the universal
CC detection of any bacterium, fungus or parasite in a sample and for the
CC detection of at least one antimicrobial agent resistance gene or at
CC least one toxin gene. hexa nucleic acids are used for the specific and
CC ubiquitous detection and for identification of Streptococcus pneumoniae.
CC (1) can be used to design a therapeutic agent which is effective against
CC microorganisms. Microbial species or genus or family or phylum or group
CC which can be detected include Abiotrophia adiacens, Bordetella sp.,
CC Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,
CC Mycobacteriaceae family, Pseudomonads group, Streptococcus sp.,
CC Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests
CC provides faster results than substrate specificity tests as results can
CC be determined in an hour and improved accuracy is also achieved.
CC AAH00010 to AAH002304 represent nucleotide sequences and primers/probes
XX which are given in the exemplification of the present invention.
XX
XX Sequence 3534 BP; 679 A; 1081 C; 1188 G; 586 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 22; Length 3534;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacggcgcttcgatgaacc 20
DB 1547 TACGGCGTTTCGATGACCC 1528
RESULT 11
```

```
AAA74651/C
ID AAA74651 standard; DNA: 3853 BP.
XX
AC AAA74651;
XX
DT 06-DEC-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene.
XX
KM Mycobacterium tuberculosis: rpoB; RNA polymerase beta subunit;
KW rifampin resistance; mutation detection; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200043546-A2.
XX
PD 27-JUL-2000.
XX
PF 20-DEC-1999; 99WO-US50377.
XX
PR 19-JAN-1999; 99US-0233996.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-524243/47.
XX
PT Method for detecting drug resistance in a strain of an organism,
PT particularly for detecting rifampin resistance in Mycobacterium
PT tuberculosis -
XX
XX
PS Example 1: Fig 4; 86pp; English.
XX
CC The present sequence is the rpoB gene from Mycobacterium tuberculosis.
CC Rifampin resistance is largely associated with point mutations
CC localised in a small core region of 81 base pairs in the rpoB gene, which
CC encodes the RNA polymerase beta subunit. To detect a mutation, a complex
CC is formed comprising a first sequence representing the predetermined
CC region of the gene of the organism and a second sequence representing the
CC corresponding region of the gene of the wild type organism in double
CC stranded form. Each member of at least one pair of non-complementary
CC strands within the complex has a label. The association of the labels in
CC the complex is related to the presence of the mutation. The presence of
CC the mutation is related to the drug resistance of the strain.
XX
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;

Query Match          100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
   |||||||
DB 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 12
AAA89994/C
ID AAA89994 standard; DNA: 3853 BP.
XX
AC AAA89994;
XX
DT 18-DEC-2000 (first entry)
XX
DE M. tuberculosis rpoB gene encoding RNA polymerase beta subunit.
XX
KM Drug resistance; rifampin; rifampicin; pyrazinamide; rpoB;
KW RNA polymerase beta subunit; ds.
XX
OS Mycobacterium tuberculosis.
XX
```

```
PN WO200043545-A2.
XX
PD 27-JUL-2000.
XX
PF 14-DEC-1999; 99WO-US29517.
XX
PR 19-JAN-1999; 99US-0233996.
PR 22-APR-1999; 99US-0236894.
XX
PA (DADE-) DADE BEHRING INC.
XX
PI Liu YP, Kurn N;
XX
DR WPI: 2000-499235/44.
XX
PT Detecting resistance of drugs such as rifampicin in strains of
PT Mycobacterium, comprising detecting mutations in a gene and relating
PT them to drug resistance -
XX
XX
PS Example 1: Fig 4; 91pp; English.
XX
CC This invention relates to a method for detecting drug resistance in a
CC strain of an organism. The method comprises detecting the presence of at
CC least 1 mutation in a first sequence and relating the presence of the
CC mutation to drug resistance. Included in the invention are a kit for
CC carrying out the method and a method for detecting the presence of a
CC difference between two related nucleic acid sequences in an organism. The
CC methods are useful for detecting resistance to drugs such as rifampin and
CC pyrazinamide in Mycobacterium. The present sequence represents the
CC Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase
CC beta subunit). The sequence is used in an example of the method of the
CC invention for the detection of rifampin resistance in M. tuberculosis.
XX
XX
SQ Sequence 3853 BP; 723 A; 1173 C; 1293 G; 664 T; 0 other;
```

```
Query Match          100.0%; Score 20; DB 21; Length 3853;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggcgcttcgatgaacc 20
   |||||||
DB 2122 TACGGCGTTTCGATGAACCC 2103

RESULT 13
AAT12096
ID AAT12096 standard; DNA: 19 BP.
XX
AC AAT12096;
XX
DT 10-JUL-1996 (first entry)
XX
DE M. tuberculosis rpoB gene fragment amplification primer p6.
XX
KM Antibiotic resistance; spectrum; gene; mycobacterium;
KW determination; amplification; tuberculosis; rpoB; fragment;
KW primer; differential; hybridisation; pattern; rifampicin;
KW rifabutin; species identification; ss.
XX
OS Synthetic.
XX
PN WO9533851-A2.
XX
PD 14-DEC-1995.
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI De Beenhouwer H, Jannes G, Machtelinx L, Portaeis F;
```

PI Rosseau R;
 XX
 DR WPI: 1996-040250/04.
 XX
 PT Probes and primers for determ. of antibiotic resistance spectrum of
 PT Mycobacterium, opt. coupled with species identification - from
 PT different patterns of hybridisation with rpoB gene
 XX
 PS Claim 22; Page 39; 69pp; English.
 XX
 CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
 CC determined by amplifying the relevant part of the antibiotic
 CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
 CC amplified using the primer set AAT12091-98, hybridising it with at
 CC least 1 rpoB gene probe, detecting the hybrids formed and
 CC interpreting the ARS, and opt. the spp., from the differential
 CC hybridisation patterns. The method is partic. useful for the
 CC detection of rifampicin and/or rifabutin resistance in M. leprae
 CC or M. tuberculosis, and mycobacterial spp. identification. The
 CC method is rapid and reliable and provides simultaneous determ.
 CC of ARS and spp. identity.
 CC
 SQ Sequence 19 BP; 4 A; 5 C; 5 G; 5 T; 0 other;
 Query Match 95.0%; Score 19; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 tacggcggttcgatgaacc 19
 Db 1 tacggcggttcgatgaacc 19
 |||||
 RESULT 14
 ID AAO51532 standard; DNA; 3447 BP.
 XX
 AC AAO51532;
 XX
 DT 17-MAY-1994 (first entry)
 XX
 DE M. leprae rpoB gene.
 XX
 KW rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
 KM mutant; ss.
 XX
 OS Mycobacterium leprae.
 XX
 FH Key location/Qualifiers
 FT CDS 1..3447
 FT /*tag= a
 FT /note= "rifampicin-sensitive; in resistant
 FT strains the Ser codon (TCG at
 FT nucleotides 1273-1275) is often mutated
 FT to a Phe, Met or esp. Leu codon"
 XX
 PN W09322454-A.
 XX
 PD 11-NOV-1993.
 XX
 PE 30-APR-1993; 93WO-EP01063.
 XX
 PR 17-SEP-1992; 92FR-0011098.
 PR 30-APR-1992; 92US-0815940.
 PR 14-AUG-1992; 92US-0929206.
 PR 16-APR-1993; 93FR-0004545.
 XX
 PA (ASST-) ASSISTANCE PUBLIQUE.
 PA (INSP-) INST. PASTEUR.
 PA (MEDT-) MEDICAL RES COUNCIL.
 PA (UYBE-) UNIV. BERNE.
 PA (UYPA-) UNIV. CURIE PARIS VI P & M.

XX
 PI Bodmer T, Cole S, Heym B, Honore N, Telenti A;
 PI Young D, Zhang Y;
 XX
 DR WPI: 1993-368812/46.
 DR P-PSDB; AAR436771.
 XX
 PT Rapid detection of antibiotic resistance in Mycobacteria - esp.
 PT isoniazid, rifampicin or streptomycin resistance in tuberculosis
 PT by detecting mutation in katG, rpoB or rpsL genes
 XX
 PS Example 2; Fig 12; 97pp; English.
 XX
 CC PCR amplification was used to obtain rpoB genes from rifampicin-
 CC resistant Mycobacterium leprae strains. A comparison with the
 CC sequence of the rpoB gene from sensitive strains (AAO51532) revealed
 CC mutations in the region encoding amino acids 400-450. A common
 CC mutation seen in resistant strains occurs at codon 425 where Ser is
 CC substituted, most frequently by Leu.
 CC
 SQ Sequence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;
 Query Match 92.0%; Score 18.4; DB 14; Length 3447;
 Best Local Similarity 95.0%; Pred. No. 3;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 tacggcggttcgatgaacc 20
 Db 1454 TACGGTGTTCGATGATGACCC 1435
 |||||
 RESULT 15
 ID AAS1357 standard; DNA; 3474 BP.
 XX
 AC AAS1357;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Enterococcus faecalis DNA for cellular proliferation protein #134.
 XX
 KW Antisense; ds; prokaryotic cellular proliferation gene;
 KM antibiotic; antibacterial; drug design.
 XX
 OS Enterococcus faecalis.
 XX
 PN W0200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PE 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELITR-) ELITRA PHARM INC.
 XX
 PI Hasselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI: 2001-611495/70.
 DR P-PSDB; AAO33498.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Claim 27; Seq ID No 3939; 511pp; English.

XX
CC The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence encodes an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
SQ Sequence 3474 BP: 1074 A; 691 C; 776 G; 933 T; 0 other;

Query Match 84.0%; Score 16.8; DB 23; Length 3474;
Best Local Similarity 90.0%; Pred. No. 21;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 tacggcggttcgattgaacc 20
|||
Db 1652 TAAGCGGTTTCGATGAACC 1633

Search completed: August 7, 2002, 22:04:01
Job time: 8061 sec

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GenCore version 4.5
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OW nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:51:37 ; Search time 2167.9 Seconds

(without alignments)
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Title: US-09-786-105-2

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Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba: *
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3: gb_in: *
4: gb_om: *
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7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mnu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
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30: em_hhg_hum: *
31: em_hhg_inh: *
32: em_hhg_other: *
33: em_hhg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

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C	2	20	100.0	432	6	AR067448	AR067448 Sequence
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C	4	20	100.0	620	6	AR062057	AR062057 Sequence
C	5	20	100.0	620	6	AR062058	AR062058 Sequence
C	6	20	100.0	620	6	AR062059	AR062059 Sequence
C	7	20	100.0	620	6	AR062060	AR062060 Sequence
C	8	20	100.0	620	6	AR062061	AR062061 Sequence
C	9	20	100.0	705	1	AF060353	AF060353 Mycobacte
C	10	20	100.0	706	6	AR149128	AR149128 Sequence
C	11	20	100.0	970	6	I50706	I50706 Sequence 1
C	12	20	100.0	3534	6	AX111339	AX111339 Sequence
C	13	20	100.0	3853	1	MRU12205	U12205 Mycobacteri
C	14	20	100.0	5084	1	MSGRIFRNAP	L27989 Mycobacteri
C	15	20	100.0	19352	1	AE006964	AE006964 Mycobacte
C	16	20	100.0	19770	1	MTC1376	295972 Mycobacteri
C	17	18.4	92.0	626	1	AF060295	AF060295 Mycobacte
C	18	18.4	92.0	703	1	AF060349	AF060349 Mycobacte
C	19	18.4	92.0	705	1	AF060279	AF060279 Mycobacte
C	20	18.4	92.0	705	1	AF060290	AF060290 Mycobacte
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C	27	18.4	92.0	705	1	AF060327	AF060327 Mycobacte
C	28	18.4	92.0	705	1	AF060328	AF060328 Mycobacte
C	29	18.4	92.0	705	1	AF060329	AF060329 Mycobacte
C	30	18.4	92.0	705	1	AF060331	AF060331 Mycobacte
C	31	18.4	92.0	705	1	AF060351	AF060351 Mycobacte
C	32	18.4	92.0	705	1	AF060356	AF060356 Mycobacte
C	33	18.4	92.0	3316	1	AF172323	AF172323 Bacillus
C	34	18.4	92.0	3447	6	AR067447	AR067447 Sequence
C	35	18.4	92.0	37617	1	MLB1790G	214314 M. lepreae ge
C	36	18.4	92.0	348950	1	MLEPRTN7	AL583923 Mycobacte
C	37	17.4	87.0	10909	1	AE007977	AE007977 Agrobacte
C	38	17.4	87.0	13047	1	AE009010	AE009010 Agrobacte
C	39	16.8	84.0	518	1	AF325874	AF325874 Staphyloc
C	40	16.8	84.0	643	1	AF060346	AF060346 Mycobacte
C	41	16.8	84.0	647	1	AF060350	AF060350 Mycobacte
C	42	16.8	84.0	652	1	AF060344	AF060344 Mycobacte
C	43	16.8	84.0	652	1	AF060364	AF060364 Mycobacte
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ALIGNMENTS

RESULT 1
LOCUS MSGRIFRNAP/c 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37) DNA.
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE
AUTHORS Teleni, A., Imboden, P., Marchesi, F., Lowrie, D., Cole, S. T.,
Colston, J., Maiter, L., Schopfer, K. and Bodmer, T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)
FEATURES
Location/Qualifiers
1..432
/organism="Mycobacterium tuberculosis"
/strain="H37"

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ORIGIN
Query Match          100.0%; Score 20; DB 1; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches   20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY       1 tacggcgcttcgatgaaccc 20
         ||| ||||| ||||| |||||
Db       428 TACGGCGCTTCGATGAACCC 409

RESULT_2
AR067448/c      AR067448      432 bp      DNA      linear      PAT 29-SEP-1999
LOCUS

```

DEFINITION	Sequence 59 from patent US 5851763.
ACCESSION	AR067448
VERSION	AR067448.1
KEYWORDS	GI:5998670
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unknown.
AUTHORS	Unclassified.
TITLE	1 (bases 1 to 432)
JOURNAL	Haym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and
FEATURES	rapid detection of antibiotic resistance in mycobacterium
source	luberdelosis
	Patent: US 5851763-A 59 22-DEC-1998;
	Location/Qualifiers
	1..432
BASE COUNT	77 a 139 c 149 g 67 t
ORIGIN	/organism="unknown"
Query Match	100.0%; Score 20; DB 6; Length 432;
Best Local Similarity	100.0%; Pred. No. 1.3;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 tacgagcgttcgatgaacc 20
Db	428 TACGGCGTTTCGATGAACCC 409
RESULT	3
LOCUS	AR062056/c
DEFINITION	Sequence 135 from patent US 5843669.
ACCESSION	AR062056
VERSION	AR062056.1
KEYWORDS	GI:5989747
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 620)
TITLE	Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
JOURNAL	Cleavage of nucleic acid acid using thermostable methanococcus
FEATURES	jannaschii FEN-1 endonucleases
source	Patent: US 5843669-A 135 01-DEC-1998;
	Location/Qualifiers
	1..620
BASE COUNT	103 a 202 c 214 g 101 t
ORIGIN	/organism="unknown"
Query Match	100.0%; Score 20; DB 6; Length 620;
Best Local Similarity	100.0%; Pred. No. 1.4;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 tacgagcgttcgatgaacc 20
Db	296 TACGGCGTTTCGATGAACCC 277
RESULT	4
LOCUS	AR062057/c
DEFINITION	Sequence 136 from patent US 5843669.
ACCESSION	AR062057
VERSION	AR062057.1
KEYWORDS	GI:5989748
SOURCE	.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 620)
TITLE	Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
JOURNAL	Cleavage of nucleic acid acid using thermostable methanococcus

JOURNAL Patent: US 5843669-A 136 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 5
AR062058/c AR062058 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 137 from patent US 5843669.
DEFINITION AR062058
ACCESSION AR062058.1 GI:5989749
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 137 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 103 a 201 c 214 g 102 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 296 TACGGCGTTTCGATGAACCC 277

RESULT 6
AR062059 AR062059 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 138 from patent US 5843669.
DEFINITION AR062059
ACCESSION AR062059.1 GI:5989750
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 138 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 101 a 214 c 202 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 7
AR062060 AR062060 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 139 from patent US 5843669.
DEFINITION AR062060
ACCESSION AR062060.1 GI:5989751
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 139 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 8
AR062061 AR062061 620 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 140 from patent US 5843669.
DEFINITION AR062061
ACCESSION AR062061.1 GI:5989752
VERSION
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 620)
AUTHORS Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
TITLE Cleavage of nucleic acid acid using thermostable methanococcus
JOURNAL Patent: US 5843669-A 140 01-DEC-1998;
FEATURES Location/Qualifiers
Source 1..620
/organism="unknown"
BASE COUNT 102 a 214 c 201 g 103 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 tacggcggttcgatgaacc 20
|||||
Db 325 TACGGCGTTTCGATGAACCC 344

RESULT 9
AF060353 AF060353 705 bp DNA linear BCT 15-MAY-1998
LOCUS Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene,
DEFINITION

partial cds.
AF060353
AF060353.1 GI:3133464

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 705)

REFERENCE
AUTHORS
TITLE

Glangeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniwski,F., Alland,D., Desmond,E., Holodniy,M., and Drenkow,J.
Simultaneous genotyping and species identification using
hybridization pattern recognition analysis of generic mycobacterium
DNA arrays
Genome Res. 8 (5), 435-448 (1998)

JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL

98248685
2 (bases 1 to 705)
Glangeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M.,
Drobniwski,F., Alland,D., Desmond,E., Holodniy,M., and Drenkow,J.
Direct Submission
Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
3380 Central Expressway, Santa Clara, CA 95051, USA

FEATURES
SOURCE

1..705
/organism="Mycobacterium tuberculosis"
/strain="ATCC27294"
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/db_xref="taxon:1773"
<1..>705
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<1..>705
/gene="rpoB"
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/protein_id="AAC38533.1"
/db_xref="GI:3133465"
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HKRLSALPGSLRERAGLEVRDHSVHGRCMPETPEPNTGLIGSLSVARVP
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EEVYVSEVDYVMVSPRQWVSATAMIPLEHDNARALMGAMQAGVPLVASEAP
LVGTGMLRAIDAT"

BASE COUNT 117 a 227 c 250 g 111 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 331 TACGGCGTTTCGATGACCC 312

RESULT 10
ARI49128/c 706 bp DNA linear PAT 08-AUG-2001

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

ARI49128
Sequence 24 from patent US 6228575.
ARI49128
ARI49128.1 GI:15113719
Unknown.
Unclassified.
1 (bases 1 to 706)
Glangeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
Ghandour,G., and Wang,C.
Chip-based species identification and phenotypic characterization
of microorganisms
Patent: US 6228575-A 24 08-MAY-2001;
Location/Qualifiers

JOURNAL
AUTHORS
TITLE
JOURNAL
FEATURES

source 1..706
/organism="unknown"
BASE COUNT 117 a 227 c 250 g 111 t 1 others
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 706;
Best Local Similarity 100.0%; Pred. No. 1.4; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
|||||
Db 332 TACGGCGTTTCGATGACCC 313

RESULT 11
150706/c 970 bp DNA linear PAT 07-OCT-1997

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

150706
Sequence 1 from patent US 5643723.
150706
150706.1 GI:2472409
Unknown.
Unclassified.
1 (bases 1 to 970)
Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., Roberts,G.D.
and Whelan,A.Christian.
Detection of a genetic locus encoding resistance to rifampin in
mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers
1..970
/organism="unknown"

BASE COUNT 182 a 302 c 330 g 156 t

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcggttcgatgaacc 20
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Db 671 TACGGCGTTTCGATGACCC 652

RESULT 12
AX111339/c 3534 bp DNA linear PAT 30-APR-2001

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AX111339
Sequence 2072 from Patent WO0123604.
AX111339
AX111339.1 GI:13927631
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriaceae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
Bergeron,M.G., Boissnot,M., Huletsky,A., m Nard,C., Ouellette,M.,
Picard,F.J., and Roy,P.H.
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072 05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
1..3534
/organism="Mycobacterium tuberculosis"
/strain="RV"
/db_xref="taxon:1773"

BASE COUNT 679 a 1081 c 1188 g 586 t

ORIGIN

	Query Match	100.0%	Score 20;	DB 6;	Length 3534;
	Best Local Similarity	100.0%	Pred. No. 1.9;		
	Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1 taaggcgcttcgatgaaccg 20				
Db	1547 TACGGCGTTTGATGAACCC 1528				

FEATURES	source
RESULT 13	
LOCUS	MTU12205/c
DEFINITION	MTU12205 3853 bp DNA linear BCT 02-MAR-2000
ACCESSION	Mycobacterium tuberculosis H37Rv RNA-polymerase Beta subunit (ipob).
VERSION	U12205
KEYWORDS	U12205.1 GI:515684
SOURCE	
ORGANISM	Mycobacterium tuberculosis.
	Mycobacterium tuberculosis
	Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
	Actinomycetales; Corynebacterineae; Mycobacteriaceae;
	Mycobacterium; Mycobacterium tuberculosis complex.
	1 (bases 1 to 3853)
REFERENCE	Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
AUTHORS	Cole, S., Schopfer, K. and Burkart, T.
	The ipob gene of Mycobacterium tuberculosis
	Unpublished
TITLE	2 (bases 1 to 3853)
JOURNAL	Imboden, P.
REFERENCE	Direct Submission
AUTHORS	Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
TITLE	Microbiology, University of Berne, Friedbuehlstrasse 51,
JOURNAL	3010, Switzerland
	Location/Qualifiers
	1..3853

BASE COUNT	723 a	1173 c	1293 g	664 t
ORIGIN				

	Query Match	100.0%	Score 20;	DB 1;	Length 3853;
	Best Local Similarity	100.0%	Pred. No. 2;		
Matches	20; Conservative	0;	Mismatches	0;	Gaps 0;
OY	1 taacgagcttcgatgaacc	20			
Db	2122 TAACGAGCTTTCATGAACC	2103			

RESULT	14
MSGRPOB/c	
LOCUS	5084 bp DNA linear BCT-13-SEP-1994
DEFINITION	Mycobacterium tuberculosis RNA polymerase beta-subunit (rpoB) gene, complete cds and RNA polymerase beta-subunit rpoC gene, partial cds.
ACCESSION	L27989
VERSION	L27989.1 GI:468333
KEYWORDS	RNA polymerase beta-subunit; rpoB gene.
SOURCE	Mycobacterium tuberculosis (strain RV) DNA.
ORGANISM	Mycobacterium tuberculosis Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 5084)
REFERENCE	Miller/L.P., Crawford,J.T. and Shinnick,T.M. The rpoB gene of Mycobacterium tuberculosis Antimicrob. Agents Chemother. 38 (4), 805-811 (1994) 94304130
AUTHORS	
TITLE	
JOURNLT	
MEDLINE	
FEATURES	Location/Qualifiers 1..5084
source	

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gene      4641..5084
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4641..5084
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/db_xref="GI:537608"

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GLFCEKIFGPTROMECYCGKYKRVFRGIIICERGCVEYTRAKVRERMGHIELAPVT
HIWFKGVPRLGILDLAPLDLEIKIITFAAYITTSVDEMRHNEL"

BASE COUNT 969 a 1534 c 1691 g 890 t

ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 5084;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 tacgagcattcgatgaacc 20
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Db 2611 TACGGCGTTTCGATGACCC 2592

RESULT 15
AE006964/c 19352 bp DNA linear BCT 27-APR-2001
LOCUS Mycobacterium tuberculosis CDC1551, section 50 of 280 of the
DEFINITION complete genome.
ACCESSION AE006964 AE000516
VERSION AE006964.1 GI:13880217
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
FEATURES
SOURCE
gene
CDS

1 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Uterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
Unpublished
2 (bases 1 to 19352)
Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., White, O., Peterson, J., Deboy, R., Dodson, R., Gwinn, M., Haft, D., Hickey, E., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Salzberg, S.L., Delcher, A., Uterback, T., Weidman, J., Khouri, H., Gill, J., Mikula, A. and Bishai, W.
Direct Submission
Submitted (25-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
1. 19352
/organism="Mycobacterium tuberculosis CDC1551"
/strain="CDC1551"
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/note="clinical strain"
163..3699
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163..3699
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TEKGTITINTEKRVVSVQVRSFVDFETIDKSTDTLHSAVIVSRGAWLEEDVK
RDIVGAVIDRRKRPQVIVLKAIGMTSEQIVERRGSEIMRSTLEKNDVTGDEALD
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EEDVVAITIEYLHNEGOTMTVPGVGEVETDDIDHFGNRLRTVGLGELTSDLT
MSMERVYRERMTOVEAITPOTLINIRPVAAIKFEFECTSOLSOQPMONNLSGIT
HKRRSLALGCGLSRERAGLEVADVHPSHIGRMCPITETPGPNTIGLIGLSVYARVNP

FGFETPYRKVVGVSDEIYVLTADDEDRVVAQANSPIADGRPRVRYLRKAG
EVEVPSSEVDYNDVSRQWVSATTAIPLEHDDNARALGAMQKQAPLVNSEAP
LVIGTGMELRAIDAGVVAEESVIEVSADYITVHNDGTRTRRYNRKFRARNHCT
CANQCPITVADGRVAGQVIVADGCTDQALVNLHVLIMPEGNHEDAIILNSR
LVDEIVTSHIEHEIDARDTKLGAEEITRDIPIINIDEVLADDEGIVAGIENED
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STPYDQAEHELELSCDLPNRDQVLDVADDAKALPDRSGSEPPYVYVGMVIT
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similarity; putative"
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HIWFKGVPRLGILDLAPLDLEIKIITFAAYITTSVDEMRHNELSTLEAEMVERK
AVEQORGELEARQKLEADLAELEAGKADARARKVDDGERMRQIRDRQAEILR
LEDIWSFTKRLAPKQILVDENLRELDYRGEFTGAMGESIQKLENDIDIAEAS
LRDYLNRGKQKRLARKLRLKVAFAQSSNIPGWALDAVYVPELRPMVOLDGGR
FATSDLDLYLRVILNRRNRRLRLDIDLAGVETIVNNEKRMLOESVDALFDNGRRPVT
GPGNRPLKSLSDLKQGRFRRMLKRDYDSRVIVVPOKLQCCPKLMAL
LEKFEVYKRLVDNLHQNITKSAKRMVRRQPVWDVYEVYIAEPVLVNAAPLTHRG
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VOELFEARVPRGAPLADVNGVRLBDEGRFVITVPPDGGGEVVYDKISKQRLVR
FKHEDGSEIRVLSGDHVEVQOQMEGSGADHEVLRVQPREVOIHLVREQVEYRAG
VSIHDKIEIVYKMLRRVITIDSGSTFPLSIDAEEEAEMRRVAVAGGAPVAG
PVMGITKASLADSMISASFOETPRVLTDAIINCSDKLNGIKXEVITIGKLIPIACT
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complement(7691..8065)
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NPRGSSRRVRRRQADGATTHYERGGCGQSGQAGVYQGRNHGPRALAMORLLIHH
GEQYQRIAGAPFVRVCVSPY"
complement(8058..9972)
/gene="Mt0698"
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is not the result of a sequencing artifact; identified by
Glimmer2; putative; conserved hypothetical protein,
authentic frameshift"
10167..10925
/gene="Mt0699"
10167..10925
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PF01261"
/codon_start=1
/transl_table=11

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/protein_id="AAK4924.1"
/db_xref="GI:13880221"
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ALKAATLPIYVHAPYLINLASANNRVRIPSRKIQEFCAAADIGAALVIGHGVAD
DNDIDGFORMKALDRLTEVPEVYLENTGSDHAMRFPDILARLMDVIGDIGICG
LDVCHTWAAAGEALDAVDRIKAITGRIDLCHMDSRREAGSGRHHANLNSGQIDPDL
LVAAVAKAGAPVICETADQGRKDDIAFLRERTGS"
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sequence similarity; putative"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1709 TACGGCGTTTCGATGAAACC 1690

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Search completed: August 7, 2002, 21:51:38
 Job time: 23873 sec

Thu Aug 8 09:35:12 2002

us-09-786-105-2.rge

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 15:14:05 : Search time 146.61 Seconds
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Perfect score: 20
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	20	100.0	306	US-09-147-935A-6	Sequence 6, Appl
4	20	100.0	306	US-09-147-935A-7	Sequence 7, Appl
5	20	100.0	306	US-09-147-935A-41	Sequence 41, Appl
6	20	100.0	306	US-09-147-935A-50	Sequence 50, Appl
7	20	100.0	432	US-08-313-185-59	Sequence 59, Appl
8	20	100.0	432	US-09-082-614A-59	Sequence 59, Appl
9	20	100.0	970	US-08-250-030-1	Sequence 1, Appl
10	20	100.0	970	PCT-US95-06790-1	Sequence 1, Appl
11	19	95.0	306	US-09-147-935A-44	Sequence 44, Appl
12	18.4	92.0	25	US-08-750-088A-30	Sequence 30, Appl
13	18.4	92.0	306	US-09-147-935A-4	Sequence 4, Appl
14	18.4	92.0	306	US-09-147-935A-9	Sequence 9, Appl
15	18.4	92.0	306	US-09-147-935A-10	Sequence 10, Appl
16	18.4	92.0	306	US-09-147-935A-20	Sequence 20, Appl
17	18.4	92.0	306	US-09-147-935A-23	Sequence 23, Appl
18	18.4	92.0	306	US-09-147-935A-45	Sequence 45, Appl
19	17.4	87.0	306	US-09-147-935A-13	Sequence 13, Appl
20	17.4	87.0	306	US-09-147-935A-16	Sequence 16, Appl
21	17.4	87.0	306	US-09-147-935A-25	Sequence 25, Appl
22	17.4	87.0	306	US-09-147-935A-31	Sequence 31, Appl
23	17.4	87.0	306	US-09-147-935A-39	Sequence 39, Appl
24	17.4	87.0	306	US-09-147-935A-43	Sequence 43, Appl
25	17.4	87.0	306	US-09-147-935A-46	Sequence 46, Appl
26	17.4	87.0	306	US-09-147-935A-47	Sequence 47, Appl
27	16.8	84.0	306	US-09-147-935A-1	Sequence 1, Appl

28	16.8	84.0	306	US-09-147-935A-8	Sequence 8, Appl
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30	15.8	79.0	306	US-09-147-935A-12	Sequence 12, Appl
31	15.8	79.0	306	US-09-147-935A-14	Sequence 14, Appl
32	15.8	79.0	306	US-09-147-935A-15	Sequence 15, Appl
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36	15.8	79.0	306	US-09-147-935A-21	Sequence 21, Appl
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38	15.8	79.0	306	US-09-147-935A-26	Sequence 26, Appl
39	15.8	79.0	306	US-09-147-935A-29	Sequence 29, Appl
40	15.8	79.0	306	US-09-147-935A-30	Sequence 30, Appl
41	15.8	79.0	306	US-09-147-935A-32	Sequence 32, Appl
42	15.8	79.0	306	US-09-147-935A-34	Sequence 34, Appl
43	15.8	79.0	306	US-09-147-935A-35	Sequence 35, Appl
44	15.8	79.0	306	US-09-147-935A-36	Sequence 36, Appl
45	15.8	79.0	306	US-09-147-935A-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-08-750-088A-70
: Sequence 70, Application US/08750088A
: Patent No. 6329138
: GENERAL INFORMATION:
: APPLICANT: DE BEENHOWER, HANS
: APPLICANT: PORTAELS, FRAN OISE
: APPLICANT: MACHTELINCKX, LIEVE
: APPLICANT: JANNES, GEERT
: APPLICANT: ROSSAU, RUDI
: TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
: TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: D.C.
: COUNTRY: US
: ZIP: 20005-3934
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/750,088A
: FILING DATE: 21-FEB-1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: GOLDSTEIN, JORGE A.
: REGISTRATION NUMBER: 29,021
: REFERENCE/DOCKET NUMBER: 1657, 0010000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 70:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 20 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: US-08-750-088A-70

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Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

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Db 1 TACGTCGCGCAGCTGATCC 20

RESULT 2
US-09-147-935A-2
; Sequence 2, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 2
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2

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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 tacggtcgcgcagctgatcc 24

RESULT 3
US-09-147-935A-6
; Sequence 6, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis
US-09-147-935A-6

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Best Local Similarity 100.0%; Pred. No. 0.24;
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RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584

; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 7
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
US-09-147-935A-41
; Sequence 41, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 41
; LENGTH: 306
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US-09-147-935A-41

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Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6
US-09-147-935A-50
; Sequence 50, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; FILE REFERENCE: 0136/0F425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228

PRIOR FILING DATE: 1998-07-28
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: KOPATIN 1.0
 SEQ ID NO 50
 LENGTH: 306
 TYPE: DNA
 ORGANISM: Mycobacterium tuberculosis
 US-09-147-935A-50

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 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgcgcgcgcgcgcgc 20
 Db 5 tacggtcgcgcgcgcgcgcgc 24

RESULT 7
 US-08-313-185-59
 Sequence 59, Application US/08313185
 Patent No. 5851763

GENERAL INFORMATION:
 APPLICANT: Heym, Beate
 APPLICANT: Cole, Stewart
 APPLICANT: Young, Douglas
 APPLICANT: Zhang, Ying
 APPLICANT: Honore, Nadine
 APPLICANT: Telenti, Amalio
 APPLICANT: Bodmer, Thomas
 TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
 TITLE OF INVENTION: In Mycobacterium Tuberculosis
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/313,185
 FILING DATE: 12-OCT-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 02356.0068-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 432 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-313-185-59

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 Best Local Similarity 100.0%; Pred. No. 0.25;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 tacggtcgcgcgcgcgcgc 20

Db 18 TACGTCGCGGAGCTGATCC 37

RESULT 8
 US-09-082-614A-59
 Sequence 59, Application US/09082614A
 Patent No. 6124098

GENERAL INFORMATION:
 APPLICANT: Heym, Beate
 APPLICANT: Cole, Stewart
 APPLICANT: Young, Douglas
 APPLICANT: Zhang, Ying
 APPLICANT: Honore, Nadine
 APPLICANT: Telenti, Amalio
 APPLICANT: Bodmer, Thomas
 TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
 TITLE OF INVENTION: In Mycobacterium Tuberculosis
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3315
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/082,614A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/313,185
 FILING DATE: 12-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Meyers, Kenneth J.
 REGISTRATION NUMBER: 25,146
 REFERENCE/DOCKET NUMBER: 02356.0068-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 59:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 432 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-082-614A-59

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OY 1 tacggtcgcgcgcgcgcgc 20
 Db 18 TACGTCGCGGAGCTGATCC 37

RESULT 9
 US-08-250-030-1
 Sequence 1, Application US/08250030
 Patent No. 5643723

GENERAL INFORMATION:
 APPLICANT: Persing, David H.
 TITLE OF INVENTION: Detection of a Genetic Locus Encoding
 Resistance to Rifampin in Mycobacterial Cultures and in

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; TITLE OF INVENTION: Clinical Specimens
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,030
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueeling, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 150.105US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-250-030-1

Query Match          100.0%; Score 20; DB 1; Length 970;
Best Local Similarity 100.0%; Pred. NO. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 261 TACGTCGCGAGCTGATCC 280

RESULT 10
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; Sequence 1, Application PC/TUS9506790
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; APPLICANT: and Hoffmann-La Roche Inc.
; TITLE OF INVENTION: Detection of a Genetic Locus Encoding
; TITLE OF INVENTION: Resistance to Rifampin
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Schwegman, Lundberg & Woessner
; STREET: 3500 IDS Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/06790
; FILING DATE: 26-MAY-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Raasch, Kevin W.
; REGISTRATION NUMBER: 35,651
; REFERENCE/DOCKET NUMBER: 150.105MO1
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; PCT-US95-06790-1

Query Match          100.0%; Score 20; DB 5; Length 970;
Best Local Similarity 100.0%; Pred. NO. 0.25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 tacggtcgagcgatgcac 20
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Db 261 TACGTCGCGAGCTGATCC 280

RESULT 11
US-09-147-935A-44
; Sequence 44, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/09425
; CURRENT APPLICATION NUMBER: US/09/147,935A
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 44
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium xenopl
US-09-147-935A-44

Query Match          95.0%; Score 19; DB 4; Length 306;
Best Local Similarity 100.0%; Pred. NO. 0.75;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 acggtcgagcgatgcac 24

RESULT 12
US-08-750-088A-30
; Sequence 30, Application US/08750088A
; Patent No. 6329138
; GENERAL INFORMATION:
; APPLICANT: DE BEENHOUWER, HANS
; APPLICANT: PORTAELS, FRAN OISE
; APPLICANT: MACHTELINCKX, LIEVE
; APPLICANT: JANNES, GEERT
; APPLICANT: ROSSAU, RUDI
; TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
; TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: US
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1      ZIP: 20005-3934
2      COMPUSER READABLE FORM:
3      MEDIUM TYPE: Floppy disk
4      COMPUTER: IBM PC compatible
5      OPERATING SYSTEM: PC-DOS/MS-DOS
6      SOFTWARE: Patentin Release #1.0, Vers
7      CURRENT APPLICATION DATA:
8      APPLICATION NUMBER: US/08/750,088A
9      FILING DATE: 21-FEB-1997
10     CLASSIFICATION:
11     ATTORNEY/AGENT INFORMATION:
12     NAME: GOLDSTEIN, JORGE A.
13     REGISTRATION NUMBER: 29,021
14     REFERENCE/DOCKET NUMBER: 1657, 00100000
15     TELECOMMUNICATION INFORMATION:
16     TELEPHONE: 202-371-2600
17     TELEFAX: 202-371-2540
18     INFORMATION FOR SEQ ID NO: 30:
19     SEQUENCE CHARACTERISTICS:
20     LENGTH: 25 base pairs
21     TYPE: nucleic acid
22     STRANDEDNESS: single
23     TOPOLOGY: linear
24     MOLECULE TYPE: CDNA
25     US-08-750-088A-30

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Query Match	92.0%	Score 18.4;	DB 4;	Length 25;
Best Local Similarity	95.0%	Pred. No. 1.4;		
Matches 19; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      1  taccgtcgcgaactgatcc 20
        |  |||||
Db      6  TTCGGTCGGCGAGCTGATCC 25

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RESULTS 13
US-09-147-935A-4
: Sequence 4, Application US/09147935A
: Patent No. 6242584
: GENERAL INFORMATION:
: APPLICANT: KOOK, Yoon-Hoh
: TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
: TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
: FILE REFERENCE: 0136/0F425
: CURRENT APPLICATION NUMBER: US/09/147, 935A
: CURRENT FILING DATE: 1999-03-19
: PRIOR APPLICATION NUMBER: PCT/KR98/00228
: PRIOR FILING DATE: 1998-07-28
: NUMBER OF SEQ ID NOS: 50
: SOFTWARE: KOPATIN 1.0
: SEQ ID NO 4
: LENGTH: 306
: TYPE: DNA
: ORGANISM: Mycobacterium aurum
US-09-147-935A-4

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Query Match	92.0%	Score	18.4	DB	4	Length	306
Best Local Similarity	95.0%	Pred. No.	1.5				
Matches	19	Conservative	0	Mismatches	1	Indels	0
						Gaps	0

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QY      1 taccgctcgcgagctgattcc 20
          ||| ||||| ||||| |||
Db      5 taccgctcgcgagctgattcc 24
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RESULT 14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:

```

1  APPLICANT:  KOOK, Yoon-Joon
2  APPLICANT:  KIM, Bum-Joon
3  TITLE OF INVENTION:  A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
4  TITLE OF INVENTION:  COMPARATIVE SEQUENCE ANALYSIS OF IP0B GENE
5  FILE REFERENCE:  0136/0F425
6  CURRENT APPLICATION NUMBER:  US/09/147,935A
7  CURRENT FILING DATE:  1999-03-19
8  PRIOR APPLICATION NUMBER:  PCT/KR98/00228
9  PRIOR FILING DATE:  1998-07-28
10 NUMBER OF SEQ ID NOS:  50
11 SOFTWARE:  KOPATIN 1.0
12 SEQ ID NO 9
13     LENGTH:  306
14     TYPE:  DNA
15 ORGANISM:  Mycobacterium celatum Type2
16 US-09-147-935A-9

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Query Match	92.0%;	Score 18.4;	DB 4;	Length 306;
Best Local Similarity	95.0%;	Pred. No. 1.5;		
Matches 19;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	tacgctcgcgagctgatcc	20
Db	5	taccgtcggcgagctgatcc	24

```

RESULT 15
; Sequence 10, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
; APPLICANT: KOOK, Yoon-Hoh
; APPLICANT: KIM, Bum-Joon
; TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
; TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
; FILE REFERENCE: 0136/0Pa25
; CURRENT APPLICATION NUMBER: US/09/147,935A
; CURRENT FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/KR98/00228
; PRIOR FILING DATE: 1998-07-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 10
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium chelonae
US-09-147-935A-10

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Query Match	92.0%	Score 18.4;	DB 4;	Length 306;
Best Local Similarity	95.0%;	Pred. No. 1.5;		
Matches 19;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0.

QY	1	tacggtcgcgagctgtatcc	20
Db	5	taccgtcgcgagctgtatcc	24

Search completed: August 7, 2002, 21:54:16
Job time: 24011 sec

RESULT 14
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:

Thu Aug 8 09:35:10 2002

us-09-786-105-1.rni

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 14:53:50 ; Search time 4103.44 Seconds
(Without alignments)
65.784 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20

Sequence: 1 tacgtcgcgcagctgaccc 20

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_estdm:*
3: em_estln:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_estc:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_iny:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18.4	92.0	130	10	BM397871 5009-0-38
2	18.4	92.0	132	10	BM396091 5009-0-17
3	18.4	92.0	134	10	BM398255 5009-0-42
4	17.4	87.0	984	12	CNS01G32
5	17	85.0	422	10	BE443802 WHE1122.B
6	17	85.0	544	10	BE445100 WHE1132.H
7	17	85.0	558	10	BE444713 WHE1137.H
8	17	85.0	610	9	BE195103 HVSMEH008
9	17	85.0	658	10	BE442518 WHE1101.H
10	16.8	84.0	828	10	BG299722 HVSME002
11	16.8	84.0	419	10	BI188703 d2e05f.r
12	16.8	84.0	606	10	BI1881973 f053f08.y
13	16.8	84.0	292	9	BI888442 ZR637-2.0
14	16.4	82.0	292	9	AM502654 UI-HF-BRO
15	16.4	82.0	338	9	AM501791 UI-HF-BRO
16	16.4	82.0	402	9	BE101908 UI-R-B01
17	16.4	82.0	460	9	AM502300 UI-HF-BRO

18	16.4	82.0	470	9	AM502130	AM502130 UI-HF-BRO
19	16.4	82.0	586	10	BM321268	BM321268 rocketfell
20	16.4	82.0	653	10	BM320964	BM320964 rocketfell
21	16.4	82.0	712	10	BM321334	BM321334 rocketfell
22	16.4	82.0	899	10	BM320891	BM320891 rocketfell
23	16	80.0	708	10	BE585978	BE585978 Est#7PT7-
24	15.8	79.0	197	6	BE59873	BE59873 P11.80.GO
25	15.8	79.0	197	10	BM318366	BM318366 P11.77.GO
26	15.8	79.0	315	10	BE419003	BE419003 WMR020.D1
27	15.8	79.0	360	10	BG412215	BG412215 OV2_39.CO
28	15.8	79.0	411	10	BG263401	BG263401 WHE2341.E
29	15.8	79.0	428	9	A1967080	A1967080 496021E08
30	15.8	79.0	451	10	C72862	C72862 C72862 Rice
31	15.8	79.0	461	10	C28055	C28055 C28055 Rice
32	15.8	79.0	493	9	BE215753	BE215753 HV_CED000
33	15.8	79.0	507	6	BE599649	BE599649 P11.78.AO
34	15.8	79.0	507	10	BM318224	BM318224 P11.79.AO
35	15.8	79.0	560	10	BG411877	BG411877 OV2_39.CO
36	15.8	79.0	565	12	A2178000	A2178000 SP_0149.A
37	15.8	79.0	597	12	BH402082	BH402082 AC-ND-156
38	15.8	79.0	605	9	AL508804	AL508804 AL508804
39	15.8	79.0	672	9	BB316372	BB316372 BB316372
40	15.8	79.0	726	12	A2359615	A2359615 IM0102G02
41	15.8	79.0	740	12	BH016284	BH016284 TDCCK39TH
42	15.8	79.0	841	10	BI544719	BI544719 603242678
43	15.8	79.0	880	10	BI911230	BI911230 603062995
44	15.8	79.0	946	10	BG475629	BG475629 602520553
45	15.8	79.0	1077	12	CNS07739	AL432187 T3 end of

ALIGNMENTS

RESULT 1
BM397871/c 130 bp mRNA linear EST 17-JAN-2002
LOCUS
DEFINITION 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM397871
VERSION BM397871.1 GI:18197924
KEYWORDS
SOURCE
ORGANISM

Tetrahymena thermophila.
Tetrahymena thermophila.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE
AUTHORS Turkewitz,A.P., Karier,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel
J., and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)

TITLE
JOURNAL
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apurkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source
Location/Qualifiers
1..130
/organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+, Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT
ORIGIN
26 a 41 c 44 g 18 t 1 others

Query Match 92.0%; Score 18.4; DB 10; Length 130;
Best Local Similarity 95.0%; Pred. No. 1.7e+02;

Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tacggtcgagcgtatcc 20
 ||| ||||| ||||| |||||
 Db 94 TACCGTCGCGAGCTGATCC 75

RESULT 2
 BM396091/c 132 bp mRNA linear EST 17-JAN-2002
 LOCUS 5009-0-11-B01.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM396091
 VERSION BM396091.1 GI:18196144
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 132)
 Turkewitz/A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology
 University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..132
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_idb="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 27 a 42 c 44 g 19 t

FEATURES
 source

Query Match 92.0%; Score 18.4; DB 10; Length 132;
 Best Local Similarity 95.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tacggtcgagcgtatcc 20
 ||| ||||| ||||| |||||
 Db 96 TACCGTCGCGAGCTGATCC 77

RESULT 3
 BM398255/c 134 bp mRNA linear EST 17-JAN-2002
 LOCUS 5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
 DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
 ACCESSION BM398255
 VERSION BM398255.1 GI:18198308
 KEYWORDS EST.
 SOURCE Tetrahymena thermophila.
 ORGANISM Tetrahymena thermophila.
 Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida; Tetrahymenina; Tetrahymena.

REFERENCE 1 (bases 1 to 134)
 Turkewitz/A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
 EST from Tetrahymena thermophila, strain CU428.1, growing cells
 Unpublished (2002)
 CONTACT: Turkewitz AP
 Molecular Genetics and Cell Biology

University of Chicago
 920 E. 58th Street, Chicago, IL 60637, USA
 Tel: 773 702 4374
 Fax: 773 702 3172
 Email: apturkew@midway.uchicago.edu
 Seq primer: T3.
 Location/Qualifiers
 1..134
 /organism="Tetrahymena thermophila"
 /strain="CU428.1"
 /db_xref="taxon:5911"
 /clone_idb="Chilcoat/Turkewitz cDNA (large fraction)"
 /note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

BASE COUNT 26 a 44 c 46 g 18 t

FEATURES
 source

Query Match 92.0%; Score 18.4; DB 10; Length 134;
 Best Local Similarity 95.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 tacggtcgagcgtatcc 20
 ||| ||||| ||||| |||||
 Db 98 TACCGTCGCGAGCTGATCC 79

RESULT 4
 CNS01GJZ/c 984 bp DNA linear GSS 01-JUN-2001
 LOCUS Anopheles gambiae GSS T7 end of clone 06016 of Notredame1 library
 DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito), genomic survey sequence.
 ACCESSION A1143232
 VERSION A1143232.1 GI:7001389
 KEYWORDS GSS.
 SOURCE African malaria mosquito.
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 1 (bases 1 to 984)
 Genoscope.
 Direct Submission
 Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqre@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 2 (bases 1 to 984)
 Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
 Direct Submission
 Submitted (16-FEB-2000) BMMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
 This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut Pasteur.

FEATURES
 source
 Location/Qualifiers
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 /organism="Anopheles gambiae"
 /strain="PEST"
 /db_xref="taxon:7165"
 /clone_idb="06016"
 /clone_lib="Notredame1"
 /note="end : T7"

BASE COUNT 272 a 236 c 241 g 232 t 3 others

Query Match 87.0%; Score 17.4; DB 12; Length 984;
 Best Local Similarity 94.7%; Pred. No. 7.4e+02;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 tacggtcgagcgtgac 19
|||||
Db 103 TACGTCGCGAGCTGATCC 85

RESULT 5
BE443802 422 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1122_B06_C12S wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1122_B06_C12, mRNA
sequence.

ACCESSION BE443802
VERSION BE443802
KEYWORDS GI:9443341
SOURCE EST.

ORGANISM
Triticum aestivum

REFERENCE
AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 422)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
Location/Qualifiers

FEATURES
source

1..422
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1122_B06_C12"
/clone_11b="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 84 a 130 c 124 g 84 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 422;
Best Local Similarity 100.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 ggtcgagcgtgac 20
|||||

Db 86 GTCGCGAGCTGATCC 102

RESULT 6
BE445100 544 bp mRNA linear EST 25-JUL-2000
LOCUS WHE1132_H08_P16S wheat etiolated seedling root normalized cDNA
DEFINITION library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
sequence.

ACCESSION BE445100
VERSION BE445100
KEYWORDS GI:9444655
SOURCE EST.

ORGANISM
Triticum aestivum

REFERENCE
AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
1 (bases 1 to 544)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
Location/Qualifiers

FEATURES
source

1..544
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
/clone_11b="Wheat etiolated seedling root normalized cDNA
library"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 121 a 173 c 132 g 118 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 544;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 4 ggtcgagcgtgac 20
|||||
Db 512 GTCGCGAGCTGATCC 528

RESULT 7
BE444713 558 bp mRNA linear EST 25-JUL-2000
LOCUS BE444713
DEFINITION WHE1137.H03.005ZS Wheat etiolated seedling root normalized cDNA
library Triticum aestivum cDNA clone WHE1137.H03.005, mRNA
sequence.
ACCESSION BE444713 GI:9444264
VERSION BE444713
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 558)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Nguyen, H.T.,
Rausch, C.J., Seaton, C.L., Tong, J.C. and Zhang, D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
unpublished (2000)
JOURNAL Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
Location/Qualifiers

FEATURES

Source 1..558

/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137.H03.005"
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library"
/tissue_type="Root"
/note="stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI. Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
protocol used was that of Soares. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 122 a 180 c 134 g 122 t
ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 558;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 4 ggtcggcagctgaccc 20
|||||
Db 514 gctcggcagctgaccc 530

BE195103 610 bp mRNA linear EST 22-OCT-2001
LOCUS BE195103
DEFINITION HVSMH0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMH0088E21f,
mRNA sequence.
ACCESSION BE195103 GI:16321083
VERSION BE195103
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM barley.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 610)
Wing, R., Close, T.J., Kleinholz, A., Wise, R., Begum, D., Frisch, D., Yu
Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
R.D., Close, S.J., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex 5-45 DAP spike cDNA library
unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.
Contact: Ming RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 238
Seq primer: AATTAACCTCCTCAATAGGG
High quality sequence stop: 563.
Location/Qualifiers

FEATURES

Source 1..610

/organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMH0088E21f"
/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVCNDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
<http://www.genome.clemson.edu/projects/barley>. To order
this clone see <http://www.genome.clemson.edu/orders> Also
see Close TJ, Wing R, Kleinholz A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(<http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html>)"

BASE COUNT 127 a 203 c 158 g 120 t 2 others
ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 610;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ggtcgagcagctgaccc 20
 ||||||||||||||||
 Db 499 GGTCCGCGAGCTGATCC 515

RESULT 9
 BE442518 658 bp mRNA linear EST 25-JUL-2000
 LOCUS BE442518
 DEFINITION library Triticum aestivum cDNA clone WHE1101_H10_019, mRNA

ACCESSION BE442518
 VERSION BE442518
 KEYWORDS EST
 SOURCE bread wheat.
 ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 658)
 Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
 Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
 The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library
 Unpublished (2000)

TITLE
 JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818

Email: oanderson@w.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stragene SK primer.

FEATURES

Location/Qualifiers
 1..658
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE1101_H10_019"
 /clone.lib="Wheat etiolated seedling root normalized cDNA
 library"
 /tissue_type="Root"
 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pluescript SK: Site_1: EcoRI; Site_2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and cefotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close Lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pluescript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."

BASE COUNT 144 a 209 c 165 g 140 t
 ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 658;
 Best Local Similarity 100.0%; Pred. No. 1e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 ggtcgagcagctgaccc 20

Db 512 GGTCCGCGAGCTGATCC 528
 ||||||||||||||||

RESULT 10
 BG299722 828 bp mRNA linear EST 17-OCT-2001
 LOCUS HVSME0021120f Hordeum vulgare seedling shoot EST library
 DEFINITION HVCNMA0001 (Cold stress) Hordeum vulgare cDNA clone HVSME0021120f,
 mRNA sequence.

ACCESSION BG299722
 VERSION BG299722
 KEYWORDS EST
 SOURCE barley.
 ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 828)
 Wing,R., Close,T.J., Kleinof,A., Wise,R., Begum,D., Frisch,D., Yu
 Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.,
 Fenton,R.D. and Main,D.
 Development of a genetically and physically anchored EST resource
 for barley genomics: Morex cold-stressed seedling shoot cDNA
 library
 Unpublished (2001)

TITLE
 JOURNAL
 COMMENT Contact: Wing RA
 Clemson University Genomics Institute
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293

Email: rwing@clemson.edu
 Total hg bases = 574
 Seq primer: AATTAACTCCTCACTAAAGG
 High quality sequence stop: 643.

FEATURES

Location/Qualifiers
 1..828
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSME0021120f"
 /clone.lib="Hordeum vulgare seedling shoot EST library
 HVCNMA0001 (Cold stress)"
 /tissue_type="Seedling shoot"
 /lab_host="TJC121"
 /note="Vector: LambdaZAP; Site_1: EcoRI; Site_2: XhoI;
 Seeds were surface sterilized then germinated under axenic
 conditions in the dark at room temperature on filter paper
 with water, nystatin and cefotaxime in covered
 crystallization dishes. Five-day old seedlings were
 incubated at 50C for 2 days. Shoots were then harvested,
 total RNA was prepared, poly(A) RNA was purified, one
 primary unamplified cDNA library was made, and 600000 pfu
 were in vivo excised to give pluescript SK(-) cDNA
 phagemids. These steps were performed in the T7 Close
 laboratory at the University of California, Riverside
 (Choi, Close, Fenton). Phagemids were plated and picked at
 the Clemson University Genomics Institute (CUGI) (Begum,
 Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
 , DNA sequencing and sequence analysis were performed at
 CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
). The sequence has been trimmed to remove vector sequence
 and contains a minimum of 100 bases of phred value 20 or
 above. For more details on library preparation and
 sequence analysis see
 http://www.genome.clemson.edu/projects/barley. To order
 this clone see http://www.genome.clemson.edu/orders Also
 see Close TJ, Wing R, Kleinof A, Wise R (2001)
 Genetically and physically anchored EST resources for
 barley genomics. Barley Genetics Newsletter 31:29-30.
 (http://wheat.pw.usda.gov/g9pages/pgn/31/cover.html)"

BASE COUNT 172 a 271 c 220 g 165 t

ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 828;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 ggtcgcgcagctgcatcc 20
 |||||||
 DB 500 GGTGCGCGAGCTGATCC 516

RESULT 11
 B1188703/c 419 bp mRNA linear EST 10-JUL-2001
 LOCUS d2e05fs.r1 Fusarium sporotrichioides Tr1 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone d2e05fs 5', mRNA
 sequence.

ACCESSION B1188703
 VERSION B1188703.1 GI:14662382
 KEYWORDS EST.
 SOURCE Fusarium sporotrichioides.
 ORGANISM Fusarium sporotrichioides.
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; Mitosporic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 419)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand, M., and Roe, B.
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Other-ESTs: d2e05fs.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marlan Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 73 2.2 g117799258|emb|CAB90 (A1355752) putative integral
 membrane prote
 Seg primer: T3
 High quality sequence stop: 107.
 Location/Qualifiers
 1..419
 /organism="Fusarium sporotrichioides"
 /strain="Tr1 10"
 /db_xref="taxon:5514"
 /clone_lib="Fusarium sporotrichioides Tr1 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"
 BASE COUNT 117 a 106 c 117 g 79 t
 ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 419;
 Best Local Similarity 90.0%; Pred. No. 1.1e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 taaggctcgagctgcatcc 20
 |||||||
 DB 114 TACGCTCAGCGAGCTGATCC 95

RESULT 12
 B1981973/c 606 bp mRNA linear EST 24-OCT-2001
 LOCUS fu33f08.y1 zebrafish adult brain Danio rerio cDNA clone 533151 5'
 DEFINITION similar to TR:Q9Y4D4 Q9Y4D4 KIAA0648 PROTEIN;; mRNA sequence.

ACCESSION B1981973
 VERSION B1981973.1 GI:16371108
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Danio.
 1 (bases 1 to 606)
 REFERENCE Clark, M., Johnson, S.L., Lebrach, H., Lee, R., Li, F., Marra, M., Eddy
 'S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood
 'K., Steptoe, M., Rheising, B., Allen, M., Bowers, Y., Person, B.,
 Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E.,
 Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
 and Wilson, R.
 TITLE Mashu zebrafish EST Project 1998
 JOURNAL Unpublished (1998)
 COMMENT Other-ESTs: fu33f08.x1
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrafish@wustl.edu
 CDNA Library Preparation: John Ngai. CDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Resourcenzentrum Primatendatabank, Berlin, Germany (web address:
 www.rzpdp.de)
 High quality sequence stop: 446.
 Location/Qualifiers
 1..606
 /organism="Danio rerio"
 /db_xref="taxon:7955"
 /clone="533151"
 /clone_lib="zebrafish adult brain"
 /sex="mixed male and female"
 /tissue_type="brain"
 /dev_stage="adult"
 /lab_host="E. coli DH10B"
 /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
 Original library was constructed in lambdaZIPLOX. Mass
 excision of the cDNA library was performed to yield
 pZIPLOX plasmids. Insert check was done in original
 library."
 BASE COUNT 209 a 133 c 139 g 125 t
 ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 606;
 Best Local Similarity 90.0%; Pred. No. 1.2e+03;
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 taaggctcgagctgcatcc 20
 |||||||
 DB 452 TACGCTCAGCGAGCTGTAC 433

RESULT 13
 B1888442/c 640 bp mRNA linear EST 12-OCT-2001
 LOCUS zF637-2-000197 zebrafish shield stage whole embryo cDNA library
 MPMGP637 Danio rerio cDNA clone MPMGP637_18E17; MPMGP637E1718 5',
 mRNA sequence.
 ACCESSION B1888442
 VERSION B1888442.1 GI:16095713
 KEYWORDS EST.
 SOURCE zebrafish.
 ORGANISM Danio rerio.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
1 (bases 1 to 640)
Clark, M., Anstard, P., Hennig, S., Johnson, S.L. and Lehrach, H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)
Contact: Hennig S
laboratory 123, dept. Lebrach
Max-Planck-Institut fuer Molekulare Genetik
Imestr.63-73, D-14195 Berlin, Germany
Tel.: +49 30 8413 1612
Fax: +49 30 8413 1380
Email: hennig@molgen.mpg.de
5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
fingerprinting
High quality sequence stop: 640.

FEATURES
source

Location/Qualifiers
1..640
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone="MPMGp637_18E17;MPMGp637E1718"
/clone_lib="Zebrafish shield stage whole embryo cDNA
library MPMGP637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XL1 blue MR"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI;
oligo-OT-Moti primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"

BASE COUNT
ORIGIN

209 a 152 c 139 g 139 t 1 others

Query Match
Best Local Similarity 84.0%; Score 16.8; DB 10; Length 640;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 taagtcgcgcagctgaccc 20
|||||
Db 541 TACGCTCGCGCTGTAC 522

RESULT 14
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AM502654 292 bp mRNA linear EST 01-MAR-2000
UI-HF-BRDP-ajx-b-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075813 5', mRNA sequence.
AM502654
AM502654.1 GI:7117309
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 292)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1..292

Query Match
Best Local Similarity 82.0%; Score 16.4; DB 9; Length 292;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acgctcgcgcagctgaccc 19
|||||
Db 46 ACGCTCGCGCTGTATC 63

RESULT 15
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AM501791 338 bp mRNA linear EST 01-MAR-2000
UI-HF-BRDP-ajm-g-11-0-UI.r1 NIH_MGC_52 Homo sapiens cDNA clone
IMAGE:3075260 5', mRNA sequence.
AM501791
AM501791.1 GI:7115654
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 338)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES
source

Location/Qualifiers
1..338
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3075260"
/clone_lib="NIH_MGC_52"
/tissue_type="lymph"
/tissue_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pRT73-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT
ORIGIN

56 a 98 c 124 g 60 t

Query Match
82.0%; Score 16.4; DB 9; Length 338;

Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 acggtcggcgagctgac 19
|||||
Db 46 ACGGTGGGCGTGTGATC 63

Search completed: August 7, 2002, 21:15:17
Job time: 2287 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 15:13:45 ; Search time 2167.9 Seconds
(without alignments)
193.058 Million cell updates/sec

Title: US-09-786-105-1
Perfect score: 20
Sequence: 1 tacgtagcgagcgatcc 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_da:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
------------	-------	-------------	--------	-------	-------------

1	20	100.0	306	1	AF057450	AF057450 Mycobacte
2	20	100.0	306	1	AF057451	AF057451 Mycobacte
3	20	100.0	306	1	AF057452	AF057452 Mycobacte
4	20	100.0	306	1	AF057453	AF057453 Mycobacte
5	20	100.0	306	1	AF057454	AF057454 Mycobacte
6	20	100.0	306	6	AR157003	AR157003 Sequence
7	20	100.0	306	6	AR157007	AR157007 Sequence
8	20	100.0	306	6	AR157008	AR157008 Sequence
9	20	100.0	306	6	AR157042	AR157042 Sequence
10	20	100.0	306	6	AR157051	AR157051 Sequence
11	20	100.0	432	1	MSGR1RNAP	MSGR1RNAP
12	20	100.0	432	6	AR067448	AR067448 Sequence
13	20	100.0	970	6	150706	Sequence 1
14	20	100.0	3534	6	AX111339	AX111339 Sequence
15	20	100.0	3853	1	MTU12205	MTU12205
16	20	100.0	5084	1	MSGR1RNAP	MSGR1RNAP
17	20	100.0	19352	1	AE006964	AE006964 Mycobacte
18	20	100.0	19770	1	MTU1376	MTU1376
19	19	95.0	306	1	AF057493	AF057493 Mycobacte
20	19	95.0	306	6	AR157045	AR157045 Sequence
21	18.4	92.0	25	6	AA7816	Sequence 30
22	18.4	92.0	306	1	AF057456	AF057456 Mycobacte
23	18.4	92.0	306	1	AF057459	AF057459 Mycobacte
24	18.4	92.0	306	1	AF057460	AF057460 Mycobacte
25	18.4	92.0	306	1	AF057471	AF057471 Mycobacte
26	18.4	92.0	306	1	AF057473	AF057473 Mycobacte
27	18.4	92.0	306	1	AF057496	AF057496 Corynebact
28	18.4	92.0	306	1	AF173087	AF173087 Mycobacte
29	18.4	92.0	306	6	AR157005	AR157005 Sequence
30	18.4	92.0	306	6	AR157010	AR157010 Sequence
31	18.4	92.0	306	6	AR157011	AR157011 Sequence
32	18.4	92.0	306	6	AR157021	AR157021 Sequence
33	18.4	92.0	306	6	AR157024	AR157024 Sequence
34	18.4	92.0	306	6	AR157046	AR157046 Sequence
35	18	90.0	87	6	AX050338	AX050338 Sequence
36	17.4	87.0	306	1	AF057463	AF057463 Mycobacte
37	17.4	87.0	306	1	AF057466	AF057466 Mycobacte
38	17.4	87.0	306	1	AF057475	AF057475 Mycobacte
39	17.4	87.0	306	1	AF057480	AF057480 Mycobacte
40	17.4	87.0	306	1	AF057489	AF057489 Mycobacte
41	17.4	87.0	306	1	AF057492	AF057492 Mycobacte
42	17.4	87.0	306	1	AF057494	AF057494 Rhodococc
43	17.4	87.0	306	1	AF057495	AF057495 Nocardi
44	17.4	87.0	306	1	AF173084	AF173084 Mycobacte
45	17.4	87.0	306	1	AF173086	AF173086 Mycobacte

ALIGNMENTS

RESULT 1
AF057450
LOCUS 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial
cgs.
AF057450
AF057450.1 GI:5902487

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mycobacterium africanum.
Mycobacterium africanum
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
Actinomycetales: Corynebacteriales: Mycobacteriaceae:
Mycobacterium: Mycobacterium tuberculosis complex.

REFERENCE

AUTHORS

Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.

TITLE

Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

JOURNAL

99262756
MEDLINE
PUBMED
10325313

REFERENCE

2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

TITLE Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
Direct Submission
JOURNAL Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
Korea

FEATURES
source Location/Qualifiers
1. 306
/organism="Mycobacterium africanum"
/strain="ATCC25420"
/db_xref="ATCC:25420"
/db_xref="taxon:33894"
<1..>306
/gene="rpoB"
<1..>306
/gene="rpoB"
/transl_table=11
/codon_start=3
/product="RNA polymerase beta"
/protein_id="A055514.1"
/db_xref="GI:5902488"
/translation="RTVGELIQNIIRVGSRMERVRMTTODVEAITPOTLINIRP
VVAIKKEFGTSOLSCFMDNNPLSGITHKRRRLSALPGLSRERAGLEVRDHPSH"

gene
CDS

BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgagctgattcc 20
|||||
Db 5 TACGTCGCGAGCTGATCC 24

RESULT 2
LOCUS AF057451 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium bovis RNA polymerase beta (rpoB) gene, partial cds.
VERSION AF057451
KEYWORDS AF057451.1 GI:5902489
SOURCE Mycobacterium bovis.
ORGANISM Mycobacterium bovis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 306)
REFERENCE
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

FEATURES
source Location/Qualifiers
1. 306
/organism="Mycobacterium bovis"
/strain="ATCC19210"
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/db_xref="taxon:1765"
<1..>306
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/gene="rpoB"
/transl_table=11
/product="RNA polymerase beta"
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/db_xref="GI:5902492"
/translation="RTVGELIQNIIRVGSRMERVRMTTODVEAITPOTLINIRP
VVAIKKEFGTSOLSCFMDNNPLSGITHKRRRLSALPGLSRERAGLEVRDHPSH"

gene
CDS

/transl_table=11
/product="RNA polymerase beta"
/protein_id="A055515.1"
/db_xref="GI:5902490"
/translation="RTVGELIQNIIRVGSRMERVRMTTODVEAITPOTLINIRP
VVAIKKEFGTSOLSCFMDNNPLSGITHKRRRLSALPGLSRERAGLEVRDHPSH"

BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgagctgattcc 20
|||||
Db 5 TACGTCGCGAGCTGATCC 24

RESULT 3
LOCUS AF057452 306 bp DNA linear BCT 17-SEP-1999
DEFINITION Mycobacterium bovis BCG strain French 1173P2 RNA polymerase beta
(rpoB) gene, partial cds.
VERSION AF057452
KEYWORDS AF057452.1 GI:5902491
SOURCE Mycobacterium bovis BCG.
ORGANISM Mycobacterium bovis BCG
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 306)
REFERENCE
AUTHORS Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence
analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

FEATURES
source Location/Qualifiers
1. 306
/organism="Mycobacterium bovis BCG"
/strain="French 1173P2"
/db_xref="taxon:33892"
<1..>306
/gene="rpoB"
<1..>306
/gene="rpoB"
/transl_table=11
/product="RNA polymerase beta"
/protein_id="A055516.1"
/db_xref="GI:5902492"
/translation="RTVGELIQNIIRVGSRMERVRMTTODVEAITPOTLINIRP
VVAIKKEFGTSOLSCFMDNNPLSGITHKRRRLSALPGLSRERAGLEVRDHPSH"

BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgcgagctgattcc 20
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Db      5  TACGCTCGCGAGCTGATCC 24

RESULT  4
LOCUS   AF057453                      306 bp  DNA  linear  BCT 17-SEP-1999
DEFINITION  Mycobacterium bovis BCG RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION  AF057453
VERSION    AF057453.1  GI:5902493
KEYWORDS
SOURCE     Mycobacterium bovis BCG.
ORGANISM   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium tuberculosis complex.
REFERENCE  1  (bases 1 to 306)
AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE      Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
JOURNAL    J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE    99262756
PUBMED     10325313
REFERENCE  2  (bases 1 to 306)
AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
TITLE      Direct Submission
            Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES
source     1..306
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            /db_xref="taxon:33892"
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            /gene="rpoB"
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            /gene="rpoB"
            /codon_start=3
            /transl_table=11
            /product="RNA polymerase beta"
            /protein_id="AAD5517.1"
            /db_xref="GI:5902494"
            /translation="RTVSELIQNIIRVGSRMRERVRERMTTQDVEAITPQILNIRP
            VVAATKEFGTSQLSQFMDQNNPLSGTLTKRRLSALGPGSLRERAGLEVRDVRHSH"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  tacgctcgcgagctgatcc 20
        |||||||
Db      5  TACGCTCGCGAGCTGATCC 24

RESULT  5
LOCUS   AF057454                      306 bp  DNA  linear  BCT 08-OCT-1999
DEFINITION  Mycobacterium tuberculosis RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION  AF057454
VERSION    AF057454.1  GI:5902495
KEYWORDS
SOURCE     Mycobacterium tuberculosis.
ORGANISM   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
            Actinomycetales; Corynebacterineae; Mycobacteriaceae;
            Mycobacterium tuberculosis complex.

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REFERENCE  1  (bases 1 to 306)
AUTHORS   Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
            Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE      Identification of mycobacterial species by comparative sequence
            analysis of the RNA polymerase gene (rpoB)
JOURNAL    J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
MEDLINE    99262756
PUBMED     10325313
REFERENCE  2  (bases 1 to 306)
AUTHORS   Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,
            Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
TITLE      Direct Submission
            Submitted (06-APR-1998) Microbiology, Seoul National University
            College of Medicine, 28 Yongsan-dong, Chongno-gu, Seoul 110-799,
            Korea
FEATURES
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            /db_xref="GI:5902496"
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BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN
Query Match 100.0%; Score 20; DB 1; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  tacgctcgcgagctgatcc 20
        |||||||
Db      5  TACGCTCGCGAGCTGATCC 24

RESULT  6
LOCUS   AR157003                      306 bp  DNA  linear  PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6242584.
ACCESSION  AR157003
VERSION    AR157003.1  GI:15125707
KEYWORDS
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1  (bases 1 to 306)
AUTHORS   Kook,Y. and Kim,B.
TITLE      Method for identifying mycobacterial species by comparative
            sequence analysis of rpoB gene
JOURNAL    Patent: US 6242584-A 2 05-JUN-2001;
            Location/Qualifiers
FEATURES
source     1..306
            /organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  tacgctcgcgagctgatcc 20
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Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 7
LOCUS ARI57007 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6242584.
ACCESSION ARI57007
VERSION ARI57007.1 GI:15125711
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y.-H. and Kim,B.-J.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 6 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 96 c 107 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcgagctgattcc 20
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Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 8
LOCUS ARI57008 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 7 from patent US 6242584.
ACCESSION ARI57008
VERSION ARI57008.1 GI:15125712
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 7 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcgagctgattcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 9
LOCUS ARI57042 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 41 from patent US 6242584.
ACCESSION ARI57042
VERSION ARI57042.1 GI:15125746
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 41 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 95 c 108 g 47 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcgagctgattcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 10
LOCUS ARI57051 306 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 50 from patent US 6242584.
ACCESSION ARI57051
VERSION ARI57051.1 GI:15125755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 306)
AUTHORS Kook,Y. and Kim,B.
TITLE Method for identifying mycobacterial species by comparative
sequence analysis of rpoB gene
JOURNAL Patent: US 6242584-A 50 05-JUN-2001;
FEATURES
source Location/Qualifiers
1..306
/organism="unknown"
BASE COUNT 56 a 94 c 108 g 48 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 306;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tacggtcgcgcgagctgattcc 20
|||||
Db 5 TACGGTCGCGAGCTGATCC 24

RESULT 11
LOCUS MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993
DEFINITION Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin
resistance gene, complete cds.
ACCESSION L05910
VERSION L05910.1 GI:149991
KEYWORDS RNA polymerase beta-subunit; rifampicin resistance.
SOURCE Mycobacterium tuberculosis (strain H37).
ORGANISM Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
REFERENCE 1 (bases 1 to 432)
AUTHORS Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,T., Matter,L., Schopfer,K. and Bodmer,T.
TITLE Detection of rifampicin-resistance mutation in Mycobacterium
tuberculosis
JOURNAL Antimicrob. Agents Chemother. 341, 647-650 (1993)

FEATURES
source location/Qualifiers
1..432
/organism="Mycobacterium tuberculosis"
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HSHYGRMCPRIEPEGPNIGLSISVYANVPFRIETPYR"
149
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188
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191
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mutation 203 T"
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Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgattcc 20
|||||
Db 18 TACGTCGCGAGCTGATCC 37

RESULT 12
AR067448
LOCUS AR067448 432 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 59 from patent US 5851763.
AR067448
ACCESSION AR067448
VERSION AR067448.1 GI:5998670
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Heym, B., Cole, S., Young, D., Zhang, Y., Honore, N., Telenti, A. and Bodmer, T.
TITLE Rapid detection of antibiotic resistance in mycobacterium tuberculosis
JOURNAL Patent: US 5851763-A 59 22-DEC-1998;
FEATURES location/Qualifiers
source 1..432
/organism="unknown"
BASE COUNT 77 a 139 c 149 g 67 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 432;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgattcc 20
|||||
Db 18 TACGTCGCGAGCTGATCC 37

RESULT 13
I50706
LOCUS I50706 970 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5643723.
ACCESSION I50706
VERSION I50706.1 GI:2472409
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 970)
AUTHORS Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmler, T.A., Roberts, G.D. and Whelan, A. Christian.
TITLE Detection of a genetic locus encoding resistance to rifampin in mycobacterial cultures and in clinical specimens
JOURNAL Patent: US 5643723-A 1 01-JUL-1997;
FEATURES location/Qualifiers
source 1..970
/organism="unknown"
BASE COUNT 182 a 302 c 330 g 156 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 970;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgattcc 20
|||||
Db 261 TACGTCGCGAGCTGATCC 280

RESULT 14
AX111339
LOCUS AX111339 3534 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 2072 from Patent W00123604.
AX111339
ACCESSION AX111339
VERSION AX111339.1 GI:13927631
KEYWORDS
SOURCE Mycobacterium tuberculosis.

ORGANISM Mycobacterium tuberculosis
Bacteria; Filicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3534)
Bergeon, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M.,
Picard, F.J., and Roy, P.H.
Highly conserved genes and their use to generate probes and primers
for detection of microorganisms
Patent: WO 0123604-A 2072-05-APR-2001;
Infectio Diagnostic (I.D.I.) INC. (CA)
Location/Qualifiers
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/organism="Mycobacterium tuberculosis"
/strain="RV"
/db_xref="taxon:1773"
BASE COUNT 679 a 1081 c 1188 g 586 t
ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 3534;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgatcc 20
|||||
Db 1137 TACGGTCGCGAGCTGATCC 1156

RESULT 15
MTU12205 3853 bp DNA linear BCT 02-MAR-2000
LOCUS Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
DEFINITION gene, partial cds.
ACCESSION U12205
VERSION U12205.1 GI:515684
KEYWORDS
SOURCE
ORGANISM Mycobacterium tuberculosis.
Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Filicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T.,
Cole, S., Schopfer, K. and Burkart, T.
The rpoB gene of Mycobacterium tuberculosis
Unpublished
2 (bases 1 to 3853)
Imboden, P.
Direct Submission
Submitted (11-JUL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Berne,
3010, Switzerland
Location/Qualifiers
1..3853
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
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576..>3853
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/db_xref="GI:7144499"
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MSLSFDPDPDVKAPYDECKDKMTYAAPLFTYAFINNTEIKSQTYMGDPFPM
TERGTFLNTEERVVSVLRSPGVFEDRTDKSTKLHSVYVIRGAMLEFDVK
RDYVGRIDKKRQPVYVLKALGWTSEQIVERFGESEIRKSTLEKDNITGTDALD
ITKLKRPGEPTKESQTLLENLFKEKRYDLARVGRYKVKRKLGLHVGEPTISSTLT

FEATURES
source
gene
CDS

EEDVVAITIELVRLHEGQTWTVPAGVEVPETDDIDHFGNRRRLRTVGEILQNIQIRWG
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EGFIETPYRKVYDVSQDGYIYTLDADEDRVVAQNSPIDADRFPEPRVLYRRKAG
EVERVPSSEVDYKDVSPRQVSVATAMIPLEHDDANPALKGAMNQRQAVPLVSEAP
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ANOCPIVDAGRVAGOVIA DGPCITDGEMLGKNLVAIMPWEGHNYEDA IILSNRL
VEEDVLTSIHHEHEIDARDTKLGAEEITRDIPNISPEVLADLDERGIVRIGAEVRDG
DIIVGKVTYPRGEMETLPEERILRAIPGEKAEVBDTSIKVPHGSGKVTIGTRVPSRED
EDELPAVNEVRYRYVAKRTISDGLAGRHGKGYIGKILPYEDNPFADTPYDI
ILNTHGVPRKRNIGQILETHLGCWAHSGMKVDAGVPDMARLPDELLERQPNATVS
TPVFDGAQEAELQGLSLCTPLPNRDVDLVADGAKAMLEDFGSGEPFPYPPVYGYVM
KLHLVYDCKIHARSTGPYMTQQPLGKAKQFGGQREGMECMQAMQAYGAAYTLQELL
TIKS"

BASE COUNT 723 a 1173 c 1293 g 664 t
ORIGIN

Query Match 100.0%; Score 20; DB 1; Length 3853;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggtcgagcagctgatcc 20
|||||
Db 1712 TACGGTCGCGAGCTGATCC 1731

Search completed: August 7, 2002, 21:51:37
Job time: 23872 sec

Thu Aug 8 09:35:10 2002

us-09-786-105-1.rge

Page 7

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 21:54:31 ; Search time 562.71 Seconds
(without alignments)
61.023 Million cell updates/sec

Title: US-09-786-105-1

Perfect score: 20
Sequence: 1 tacgctgcgcagctgctatcc 20

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 45 summaries

Database:

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- 19: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
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- 21: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	Description
1	20	100.0	20	M. tuberculosis rp
2	20	100.0	20	Mycobacterium tube
3	20	100.0	20	Mycobacterium tube
4	20	100.0	20	Mycobacterium tube
5	20	100.0	20	Mycobacterium tube
6	20	100.0	20	Mycobacterium tube
7	20	100.0	20	Mycobacterium tube
8	20	100.0	20	Mycobacterium tube
9	20	100.0	20	Mycobacterium tube

10	20	100.0	306	24	AAS99530	Mycobacterium spec
11	20	100.0	306	24	AAS99531	Mycobacterium spec
12	20	100.0	432	14	AA061457	Mycobacterium rpo
13	20	100.0	480	21	AAA49863	Mycobacterium tube
14	20	100.0	970	21	AA09676	Mycobacterium tube
15	20	100.0	3519	22	AAH51976	Mycobacterium tube
16	20	100.0	3534	22	AAH02079	Mycobacterium tube
17	20	100.0	3853	21	AAA74651	Mycobacterium tube
18	20	100.0	3853	21	AAH89994	M. tuberculosis ip
19	19	95.0	306	19	AAH27217	RpoB gene fragment
20	19	95.0	306	24	AAS99551	Mycobacterium spec
21	19	95.0	21500	23	AAS59633	Propionibacterium
22	18	90.0	25	17	AAH12091	M. tuberculosis ip
23	18	90.0	87	22	AAH89922	Mycobacterium tube
24	16	80.0	306	19	AAH27212	RpoB gene fragment
25	16	80.0	306	19	AAH27218	RpoB gene fragment
26	16	80.0	306	19	AAH27193	RpoB gene fragment
27	16	80.0	306	19	AAH27196	RpoB gene fragment
28	16	80.0	306	19	AAH27204	RpoB gene fragment
29	16	80.0	306	19	AAH27177	RpoB gene fragment
30	16	80.0	306	19	AAH27182	RpoB gene fragment
31	16	80.0	306	19	AAH27183	RpoB gene fragment
32	16	80.0	306	19	AAH27186	RpoB gene fragment
33	16	80.0	306	24	AAS99539	Mycobacterium spec
34	16	80.0	306	24	AAS99557	Mycobacterium spec
35	16	80.0	306	24	AAS99560	Mycobacterium spec
36	16	80.0	306	24	AAS99565	Mycobacterium spec
37	16	80.0	306	24	AAS99568	Mycobacterium spec
38	16	80.0	27426	23	AAS59541	Propionibacterium
39	15	75.0	1092	22	AAS02316	B. subtilis DNA en
40	15	75.0	2488	23	ABL14021	Pseudomonas aerugi
41	15	75.0	2772	23	AAS54170	Drosophila melano
42	15	75.0	4544	23	ABL14020	Mycobacterium mel
43	15	75.0	4403765	22	AA199683	Mycobacterium tube
44	15	75.0	4411529	22	AA199682	Mycobacterium tube
45	14	70.0	50	19	AAV31045	Expression vector

ALIGNMENTS

XX	RESULT 1	
XX	AA12092	
XX	ID	AA12092 standard; DNA; 20 BP.
XX	AC	AA12092;
XX	DT	10-JUL-1996 (first entry)
XX	DE	M. tuberculosis rpoB gene fragment amplification primer P2.
XX	KW	Antibiotic; resistance; spectrum; gene: mycobacterium;
XX	KW	determination; amplification; tuberculosis; rpoB; fragment
XX	KW	primer; differential; hybridisation; pattern; rifampicin;
XX	KW	ribbutin; species identification; ss.
XX	OS	Synthetic.
XX	PN	
XX	XX	
XX	PD	14-DEC-1995.
XX	PE	09-JUN-1995; 95WO-EP02230.
XX	PR	09-JUN-1994; 94EP-0870093.
XX	PA	(INNO-) INNOGENETICS NV.
XX	PI	De Beenhouwer H, Jannes G, Machtelinckx L, Portael F;
XX	PI	Rossau R;
XX	DR	WPI; 1996-040250/04.
XX	XX	

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PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene

XX Claim 22, Page 39, 69pp; English.

CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp. from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

QY Query Match

Best Local Similarity 100.0%; Score 20; DB 17; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tacgctgcgcgagctgattcc 20

1 tacgctgcgcgagctgattcc 20

RESULT 2

AAA49823 standard; DNA; 20 BP.

AC AAA49823;

25-SEP-2000 (first entry)

Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

OS Mycobacterium tuberculosis.

PN MO200036142-A1.

22-JUN-2000.

10-DEC-1999; 99MO-CA01177.

11-DEC-1998; 98US-0111794.

(VIST-) VISIBLE GENETICS INC.

Shipman R;

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium

tuberculosis with antibiotic resistance in a sample -

Claim 4; Page 4; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
CC 2201-2220). It is used with the reverse primer given in AAA49824
CC and with the sequencing primers given in AAA49825 and AAA49826 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.

CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.

CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.

CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the

CC presence of antibiotic resistance-associated mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to

XX antibiotic treatment options.

XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

QY Query Match

Best Local Similarity 100.0%; Score 20; DB 21; Length 20;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 tacgctgcgcgagctgattcc 20

1 tacgctgcgcgagctgattcc 20

RESULT 3

AAA49825 standard; DNA; 20 BP.

AC AAA49825;

25-SEP-2000 (first entry)

Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.

Antibiotic resistance; rpoB gene; rifampin resistance; primer;

OS Mycobacterium tuberculosis.

PN MO200036142-A1.

22-JUN-2000.

10-DEC-1999; 99MO-CA01177.

11-DEC-1998; 98US-0111794.

(VIST-) VISIBLE GENETICS INC.

Shipman R;

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium

tuberculosis with antibiotic resistance in a sample -

Claim 4; Page 5; 43pp; English.

CC The present sequence is that of the Mycobacterium tuberculosis
CC rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
CC 2201-2220). It is used with the reverse primer given in AAA49826 and
CC with the amplification primers given in AAA49823 and AAA49824 for the
CC detection and analysis of antibiotic resistance-associated mutations
CC of the rpoB gene (see AAA49863). Amplification and cycle sequencing
CC primers (see AAA49823-62) have been developed for the detection and
CC analysis of antibiotic resistance-associated mutations in defined
CC regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc PR
CC (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

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OS Synthetic.
XX
PN [REDACTED]
XX 14-DEC-1995.
PD
XX
PF 09-JUN-1995; 95WO-EP02230.
XX
PR 09-JUN-1994; 94EP-0870093.
XX
PA (INNO-) INNOGENETICS NY.
PI De Beenhouwer H, Jannes G, Machtelincx L, Portaeals F,
PI Rossau R;
DR WPI; 1996-040250/04.
XX

THIS PAGE IS BLANK

PT Probes and primers for determ. of antibiotic resistance spectrum of
PT Mycobacterium, opt. coupled with species identification - from
PT different patterns of hybridisation with rpoB gene
PS
XX Claim 22: Page 39: 69pp: English.
CC The antibiotic resistance spectrum (ARS) of a mycobacterium can be
CC determined by amplifying the relevant part of the antibiotic
CC resistance gene, i.e. the M. tuberculosis rpoB gene fragment
CC amplified using the primer set AAT12091-98, hybridising it with at
CC least 1 rpoB gene probe, detecting the hybrids formed and
CC inferring the ARS, and opt. the spp. from the differential
CC hybridisation patterns. The method is partic. useful for the
CC detection of rifampicin and/or rifabutin resistance in M. leprae
CC or M. tuberculosis, and mycobacterial spp. identification. The
CC method is rapid and reliable and provides simultaneous determ.
CC of ARS and spp. identity.
XX
XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacgctgcgcgagctgctc 20
Db 1 tacgctgcgcgagctgctc 20

RESULT 2
AAA49823
ID AAA49823 standard; DNA: 20 BP.
AC
XX AAA49823;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;
XX ss.
OS Mycobacterium tuberculosis.
XX
XX WO200036142-A1.
XX
XX 22-JUN-2000.
XX
XX 10-DEC-1999; 99WO-CA01177.
XX
XX 11-DEC-1998; 98US-0111794.
XX
XX (VISI-) VISIBLE GENETICS INC.
XX
XX Shipman R;
XX
XX WPI: 2000-431611/37.
XX
XX Method for the detection and characterization of Mycobacterium
XX tuberculosis with antibiotic resistance in a sample -
XX
XX Claim 4; Page 4: 43pp: English.
XX
XX The present sequence is that of the Mycobacterium tuberculosis
XX rpoB (rifampin resistance) gene amplification primer rpoB-F (bp
XX 2201-2220). It is used with the reverse primer given in AAA49824
XX and with the sequencing primers given in AAA49825 and AAA49826 for the
XX detection and analysis of antibiotic resistance-associated mutations
XX of the rpoB gene (see AAA49863). Amplification and cycle sequencing
XX primers (see AAA49823-62) have been developed for the detection and
XX analysis of antibiotic resistance-associated mutations in defined
XX regions of rpoB (rifampin), katG (isoniazid), oxyr-aphc PR

CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
CC (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
CC These primers can be used in a method for the detection and
CC characterization of M. tuberculosis present in a sputum sample.
CC The method involves performing a sequencing procedure, with or
CC without prior amplification, to detect the presence of M.
CC tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
CC and 23S genes for the presence of antibiotic-inducing mutations.
CC If M. tuberculosis is detected, a second sequencing procedure is
CC performed on the sample to evaluate additional genes for the
CC presence of antibiotic resistance-inducing mutations. Genotypic
CC tests are rapid, sensitive and accurate providing information as to
CC antibiotic treatment options.
XX
XX Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;
SQ
Query Match 100.0%; Score 20; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 tacgctgcgcgagctgctc 20
Db 1 tacgctgcgcgagctgctc 20

RESULT 3
AAA49825
ID AAA49825 standard; DNA: 20 BP.
AC
XX AAA49825;
XX
DT 25-SEP-2000 (first entry)
XX
DE Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5S.
XX
KM Antibiotic resistance; rpoB gene; rifampin resistance; primer;
XX ss.
OS Mycobacterium tuberculosis.
XX
XX WO200036142-A1.
XX
XX 22-JUN-2000.
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XX 10-DEC-1999; 99WO-CA01177.
XX
XX 11-DEC-1998; 98US-0111794.
XX
XX (VISI-) VISIBLE GENETICS INC.
XX
XX Shipman R;
XX
XX WPI: 2000-431611/37.
XX
XX Method for the detection and characterization of Mycobacterium
XX tuberculosis with antibiotic resistance in a sample -
XX
XX Claim 4; Page 5: 43pp: English.
XX
XX The present sequence is that of the Mycobacterium tuberculosis
XX rpoB (rifampin resistance) gene sequencing primer rpoB-5S (bp
XX 2201-2220). It is used with the reverse primer given in AAA49826
XX and with the amplification primers given in AAA49823 and AAA49824 for the
XX detection and analysis of antibiotic resistance-associated mutations
XX of the rpoB gene (see AAA49863). Amplification and cycle sequencing
XX primers (see AAA49823-62) have been developed for the detection and
XX analysis of antibiotic resistance-associated mutations in defined
XX regions of rpoB (rifampin), katG (isoniazid), oxyr-aphc PR
XX (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
XX (streptomycin), emdB (ethambutol), pncA (pyrazinamide), gyrA
XX (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:45 ; Search time 147.68 seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-2

Perfect score: 20

Sequence: 1 tacggcgttcgattgacc 20

Scoring table: OLIGO_NUC
Gapex 60.0, Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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- 3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/1na/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/1na/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	20	100.0	432	3 US-09-082-614A-59	Sequence 59, App1
3	20	100.0	620	2 US-08-757-653-135	Sequence 135, App
4	20	100.0	620	2 US-08-757-653-136	Sequence 136, App
5	20	100.0	620	2 US-08-757-653-137	Sequence 137, App
6	20	100.0	620	2 US-08-757-653-138	Sequence 138, App
7	20	100.0	620	2 US-08-757-653-139	Sequence 139, App
8	20	100.0	620	2 US-08-757-653-140	Sequence 140, App
9	20	100.0	620	2 US-08-757-653-140	Sequence 140, App
10	20	100.0	970	1 US-08-797-812-24	Sequence 24, App1
11	20	100.0	970	5 PCT-US95-06790-1	Sequence 1, App1
12	19	95.0	19	4 US-08-750-088A-71	Sequence 1, App1
13	15	75.0	27	1 US-08-250-030-9	Sequence 9, App1
14	15	75.0	27	5 PCT-US95-06790-9	Sequence 9, App1
15	14	70.0	3447	2 US-08-313-185-57	Sequence 57, App1
16	14	70.0	3447	3 US-09-082-614A-57	Sequence 57, App1
17	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
18	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
19	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
20	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
21	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
22	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
23	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
24	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
25	13	65.0	383	3 US-08-906-769-169	Sequence 169, App
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28	13	65.0	537	4 US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4 US-09-232-200-29	Sequence 29, App1
30	13	65.0	1938	4 US-09-232-197-29	Sequence 29, App1
31	13	65.0	1938	4 US-09-232-201-29	Sequence 29, App1
32	13	65.0	3000	2 US-08-896-344A-1	Sequence 1, App1
33	13	65.0	3000	4 US-09-360-682A-1	Sequence 1, App1
34	13	65.0	3217	4 US-09-232-200-64	Sequence 64, App1
35	13	65.0	3217	4 US-09-232-197-64	Sequence 64, App1
36	13	65.0	3217	4 US-09-232-201-64	Sequence 64, App1
37	13	65.0	4403765	4 US-09-103-840A-2	Sequence 2, App1
38	12	60.0	391	1 US-08-636-928-6	Sequence 6, App1
39	12	60.0	412	4 US-08-976-259-123	Sequence 123, App
40	12	60.0	645	1 US-08-459-586-19	Sequence 19, App1
41	12	60.0	645	2 US-08-282-696-19	Sequence 19, App1
42	12	60.0	648	5 PCT-US95-04648-4	Sequence 4, App1
43	12	60.0	709	1 US-08-459-586-20	Sequence 20, App1
44	12	60.0	709	2 US-08-282-696-20	Sequence 20, App1
45	12	60.0	728	4 US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/c
Sequence 59, Application US/08313185
Patent No. 5851763

GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenfi, Amalia
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farbow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-313-185-59

Query Match 100.0%; Score 20; DB 2; Length 432;

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Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
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DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 2

US-09-082-614A-59/c

Sequence 59, Application US/09082614A

Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate

APPLICANT: Cole, Stewart

APPLICANT: Young, Douglas

APPLICANT: Zhang, Ying

APPLICANT: Honore, Nadine

APPLICANT: Telenti, Amalio

APPLICANT: Bodmer, Thomas

TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance

TITLE OF INVENTION: In Mycobacterium Tuberculosis

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: Finegan, Henderson, Farabow, Garrett &

ADDRESS: Dunner

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/082,614A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/313,185

FILING DATE: 12-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 02356, 0068-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:

LENGTH: 432 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20

|||||

DB 428 TACGGCGTTTCGATGAACCC 409

RESULT 3

US-08-757-653-135/c

Sequence 135, Application US/08757653

Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,653

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ingolia, Diane E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: FORS-02565

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 135:

SEQUENCE CHARACTERISTICS:

LENGTH: 620 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;

Best Local Similarity 100.0%; Pred. No. 0.00054;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20

|||||

DB 296 TACGGCGTTTCGATGAACCC 277

RESULT 4

US-08-757-653-136/c

Sequence 136, Application US/08757653

Patent No. 5843669

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.

APPLICANT: Lyamichev, Victor I.

APPLICANT: Lyamichev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using

TITLE OF INVENTION: Thermostable FEN-1 Endonucleases

NUMBER OF SEQUENCES: 190

CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: California

COUNTRY: United States Of America

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 7, 2002, 23:51:52 ; Search time 147.68 seconds
(without alignments)
33.266 Million cell updates/sec

Title: US-09-786-105-4

Perfect score: 20

Sequence: 1 taccgcttcgatgacc 20

Scoring table: OLIGO_NUC

Gapop 60.0, Gapext 60.0

Searched: 38353 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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6: /cgn2_6/ptodata/2/1na/Backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	432	2	US-08-313-185-59
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3	20	100.0	620	2	US-08-757-653-135
4	20	100.0	620	2	US-08-757-653-136
5	20	100.0	620	2	US-08-757-653-137
6	20	100.0	620	2	US-08-757-653-138
7	20	100.0	620	2	US-08-757-653-139
8	20	100.0	620	2	US-08-757-653-140
9	20	100.0	706	4	US-08-797-812-24
10	20	100.0	970	1	US-08-250-030-1
11	20	100.0	970	1	PCP-US95-06790-1
12	19	95.0	19	4	US-08-750-088A-71
13	19	95.0	27	1	US-08-250-030-9
14	15	75.0	27	5	PCP-US95-06790-9
15	14	70.0	3447	2	US-08-313-185-57
16	14	70.0	3447	2	US-09-082-614A-57
17	13	65.0	383	3	US-08-906-769-169
18	13	65.0	383	3	US-08-906-769-169
19	13	65.0	383	3	US-08-639-075A-169
20	13	65.0	383	4	US-09-012-431-169
21	13	65.0	383	4	US-09-012-692-169
22	13	65.0	383	4	US-08-906-613-169
23	13	65.0	537	3	US-08-906-769-171
24	13	65.0	537	3	US-08-906-616-171
25	13	65.0	537	3	US-08-639-075A-171
26	13	65.0	537	4	US-09-012-431-171
27	13	65.0	537	4	US-09-012-692-171

28	13	65.0	537	4	US-08-906-613-171	Sequence 171, App
29	13	65.0	1938	4	US-09-232-200-29	Sequence 29, App1
30	13	65.0	1938	4	US-09-232-197-29	Sequence 29, App1
31	13	65.0	1938	4	US-09-232-201-29	Sequence 29, App1
32	13	65.0	3000	2	US-08-896-344A-1	Sequence 1, App1
33	13	65.0	3000	4	US-09-360-682A-1	Sequence 1, App1
34	13	65.0	3217	4	US-09-232-200-64	Sequence 64, App1
35	13	65.0	3217	4	US-09-232-197-64	Sequence 64, App1
36	13	65.0	3217	4	US-09-232-201-64	Sequence 64, App1
37	13	65.0	4403765	4	US-09-103-840A-2	Sequence 2, App1
38	12	60.0	391	1	US-08-636-928-6	Sequence 6, App1
39	12	60.0	412	4	US-08-976-259-123	Sequence 123, App
40	12	60.0	645	1	US-08-459-586-19	Sequence 19, App1
41	12	60.0	645	2	US-08-282-696-19	Sequence 19, App1
42	12	60.0	648	5	PCT-US96-04648-4	Sequence 4, App1
43	12	60.0	709	1	US-08-459-586-20	Sequence 20, App1
44	12	60.0	709	2	US-08-282-696-20	Sequence 20, App1
45	12	60.0	728	4	US-08-998-416-615	Sequence 615, App

ALIGNMENTS

RESULT 1
US-08-313-185-59/C
Sequence 59, Application US/08313185
Patent No. 581763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenli, Amalia
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-59
Query Match 100.0%; Score 20; DB 2; Length 432;

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Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGACCC 409

RESULT 2

US-09-082-614A-59/c
; Sequence 59, Application US/09082614A
; Patent No. 6124098

GENERAL INFORMATION:

APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenit, Amelio
APPLICANT: Bodmer, Thomas

TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:

ADDRESSEE: Flunegan, Henderson, Farbow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356, 0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59

Query Match 100.0%; Score 20; DB 3; Length 432;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 428 TACGGCGTTTCGATGACCC 409

RESULT 3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843569

GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichiev, Victor I.
APPLICANT: Lyamichiev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
US-08-757-653-135

Query Match 100.0%; Score 20; DB 2; Length 620;
Best Local Similarity 100.0%; Pred. No. 0.00054;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tacggcgttcgatgaacc 20
|||||
DB 296 TACGGCGTTTCGATGACCC 277

RESULT 4
US-08-757-653-136/c
; Sequence 136, Application US/08757653
; Patent No. 5843569

GENERAL INFORMATION:

APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichiev, Victor I.
APPLICANT: Lyamichiev, Natasha

TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:

ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
ZIP: 94104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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